Figure 1A:

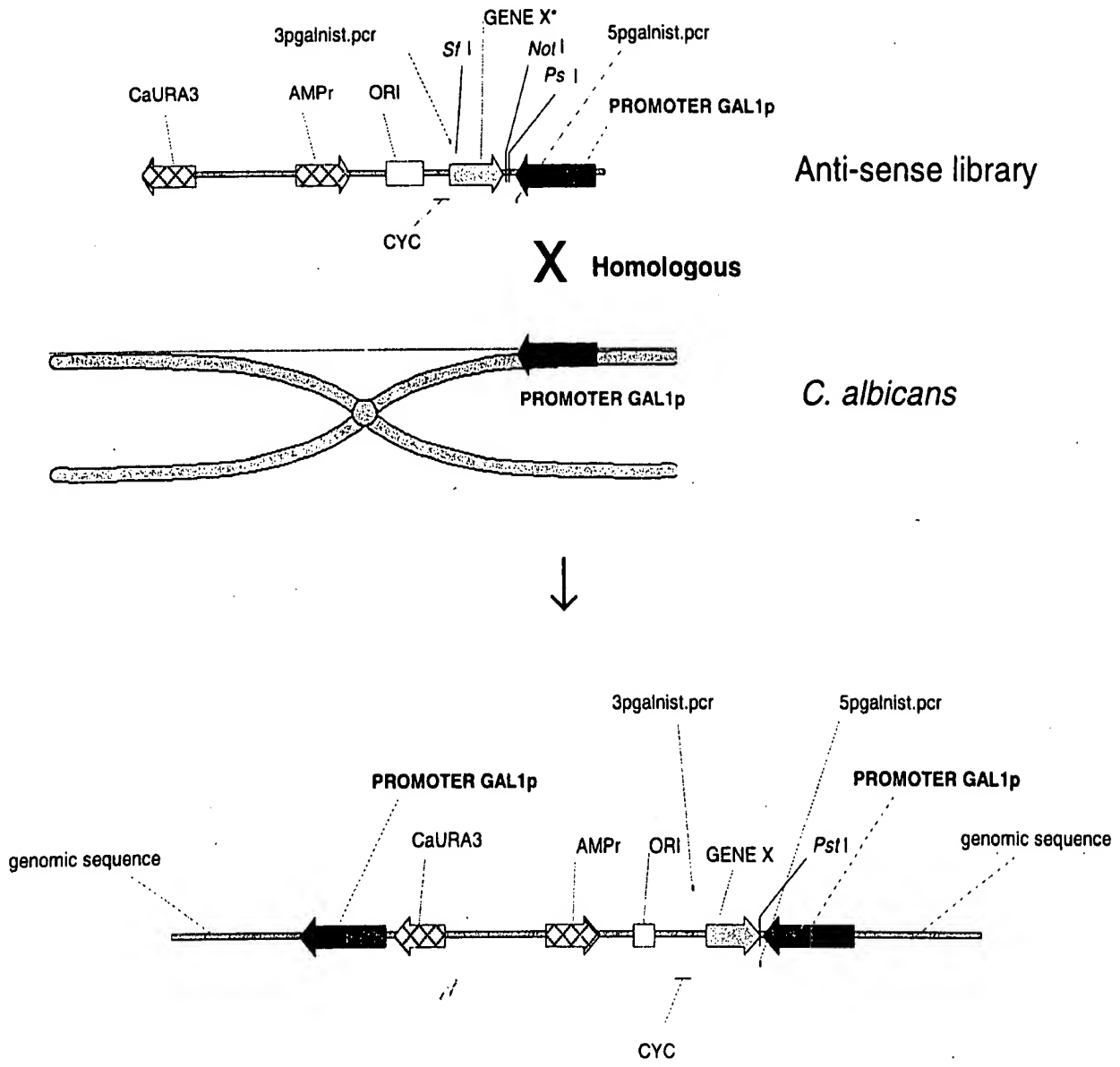

3pgalnist.pcr
GENE X*
Sf I
Not I
Ps I
5pgalnist.pcr
CaURA3
AMPr
ORI
PROMOTER GAL1p
CYC
Anti-sense library
X Homologous
PROMOTER GAL1p
C. albicans
3pgalnist.pcr
5pgalnist.pcr
PROMOTER GAL1p
PROMOTER GAL1p
genomic sequence
CaURA3
AMPr
ORI
GENE X
Pst I
genomic sequence
CYC

Figure 1B:

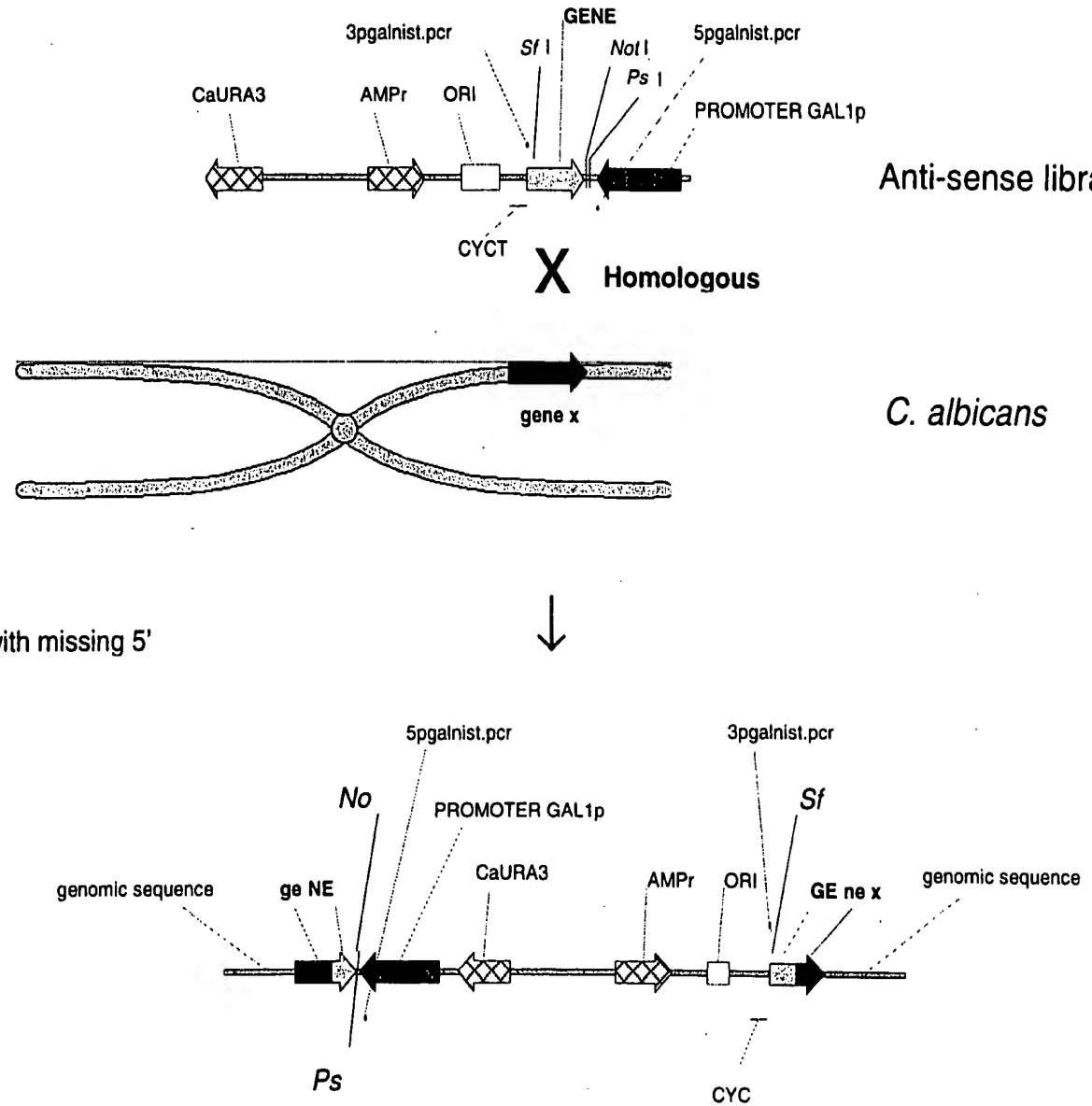


FIG. 2(a)

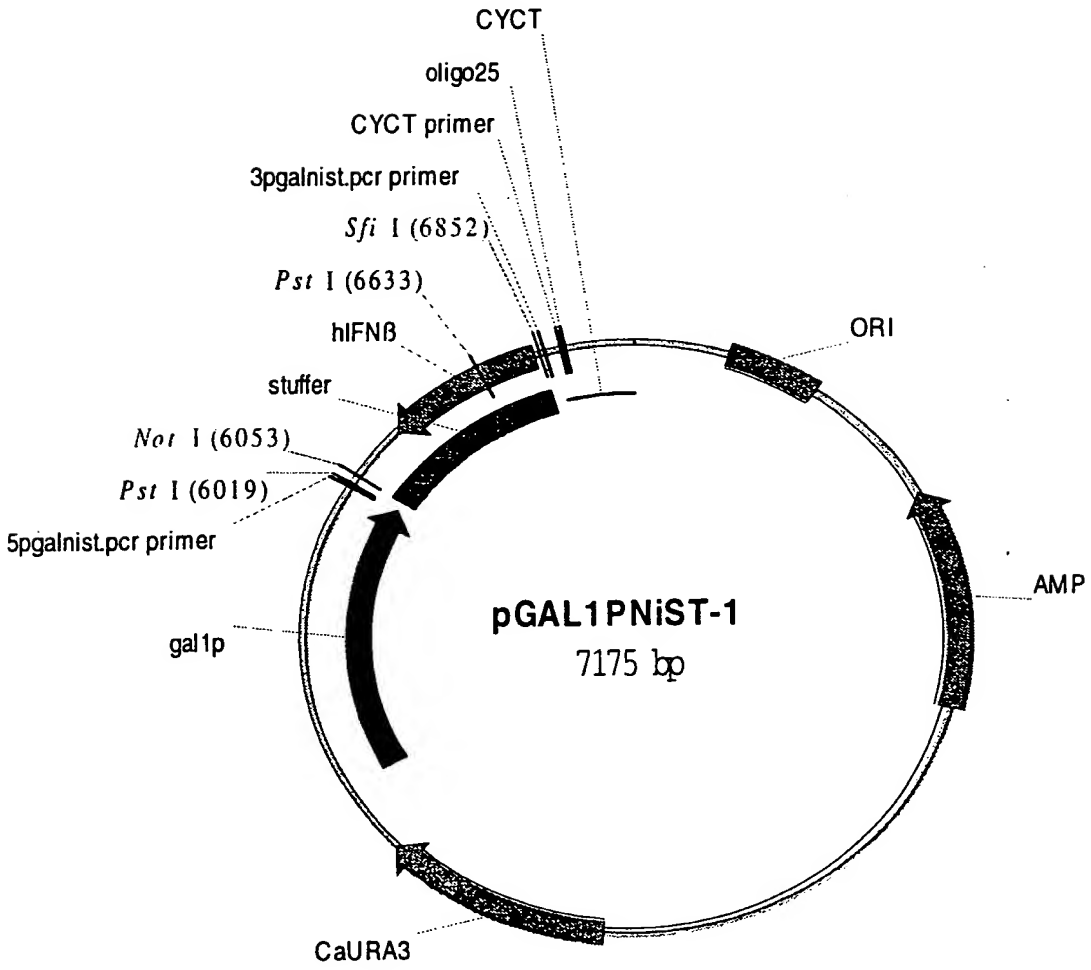
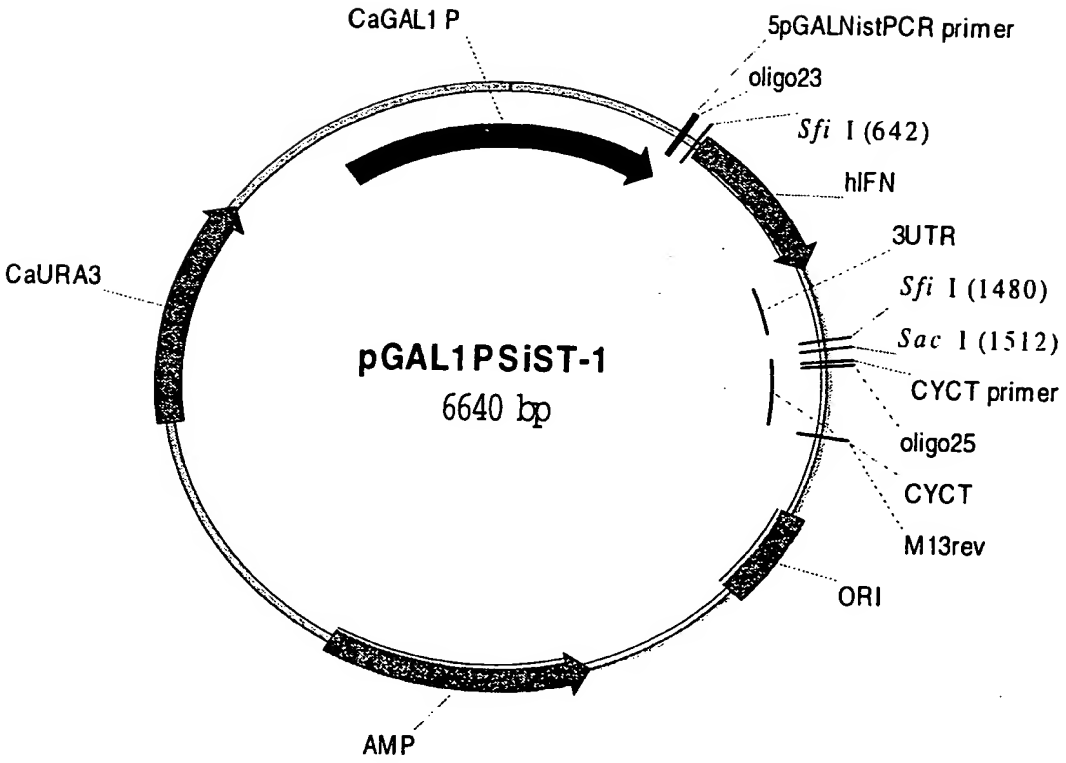
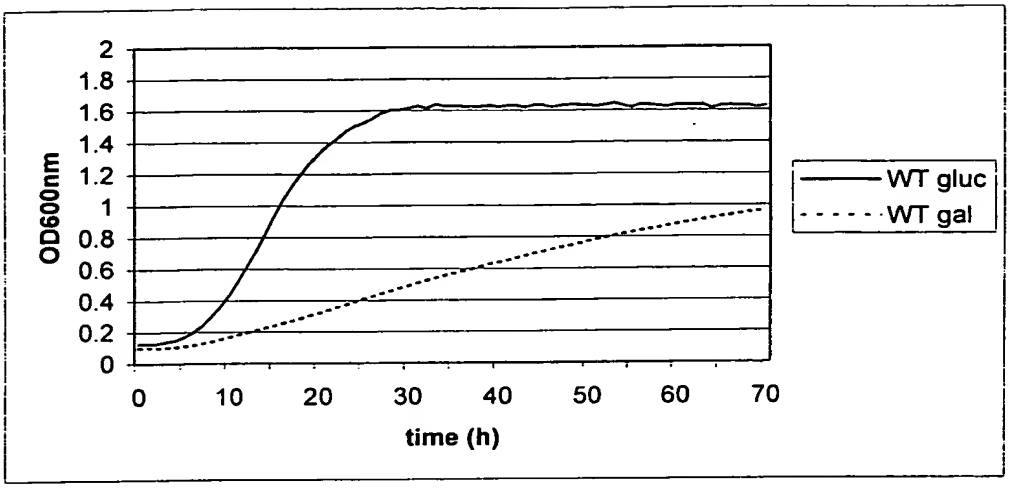
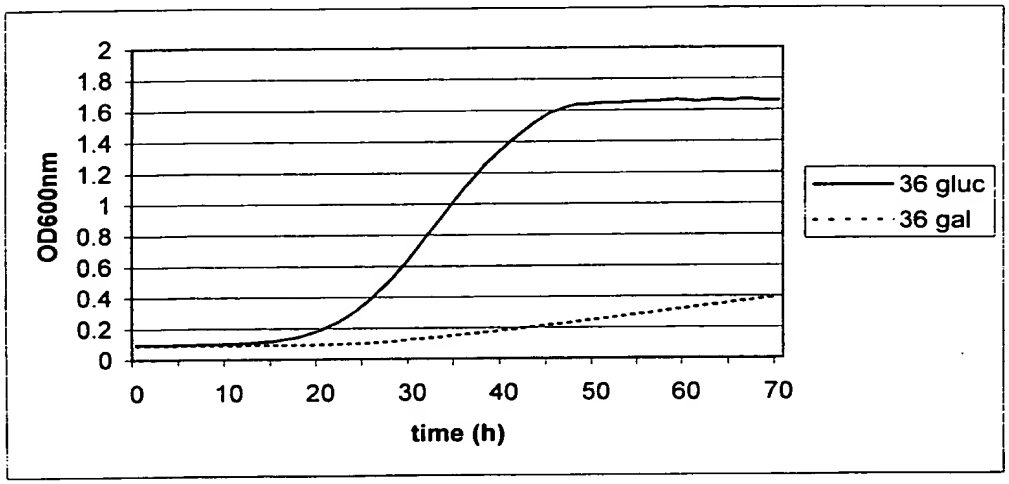

CYCT
oligo25
CYCT primer
3pgalnist.pcr primer
Sfi I (6852)
Pst I (6633)
hIFNß
stuffer
Not I (6053)
Pst I (6019)
5pgalnist.pcr primer
gal1p
ORI
AMP
CaURA3
pGAL1PNiST-1
7175 bp

FIG. 2(b)


CaGAL1 P
5pGALNistPCR primer
oligo23
Sfi I (642)
hIFN
3UTR
Sfi I (1480)
Sac I (1512)
CYCT primer
oligo25
CYCT
M13rev
ORI
AMP
CaURA3
pGAL1PSiST-1
6640 bp


OD600nm
2
1.8
1.6
1.4
1.2
1
0.8
0.6
0.4
0.2
0
0
10
20
30
40
50
60
70
time (h)
WT gluc
WT gal


OD600nm
2
1.8
1.6
1.4
1.2
1
0.8
0.6
0.4
0.2
0
0
10
20
30
40
50
60
70
time (h)
36 gluc
36 gal

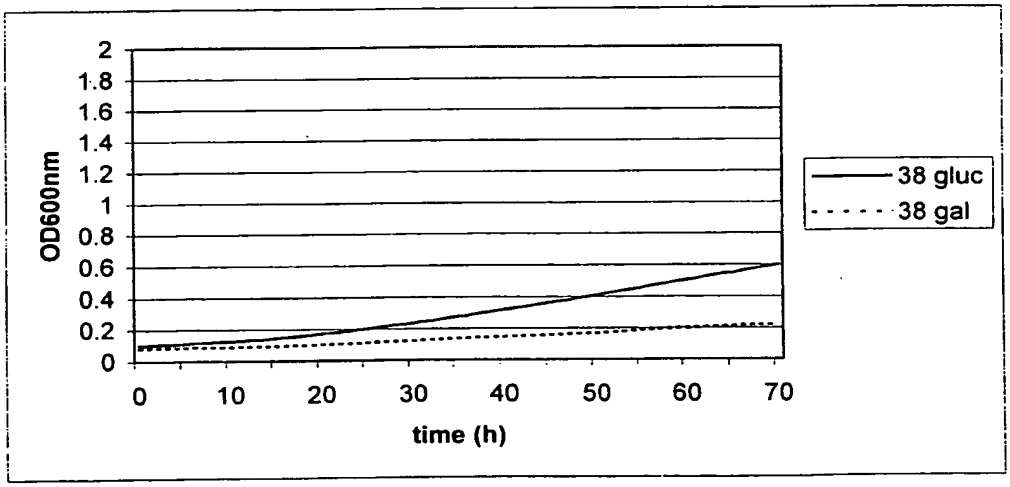
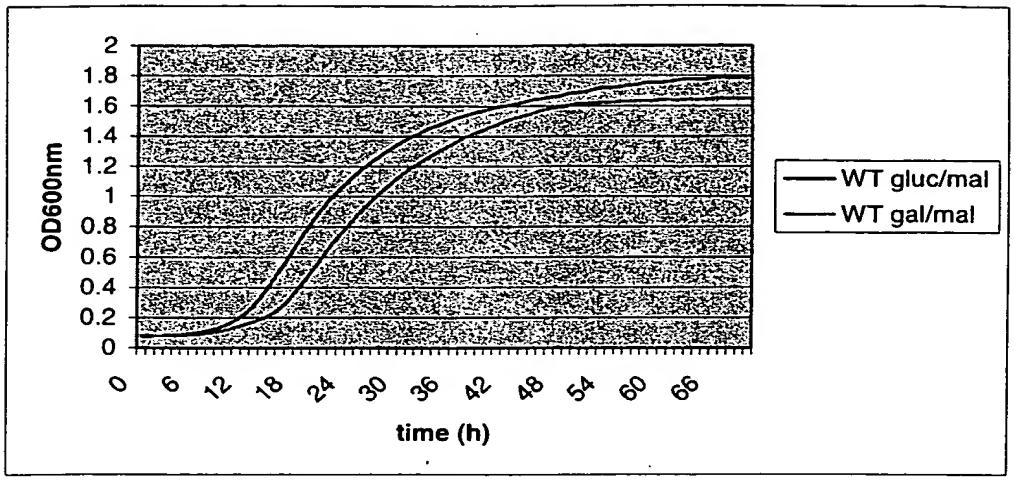
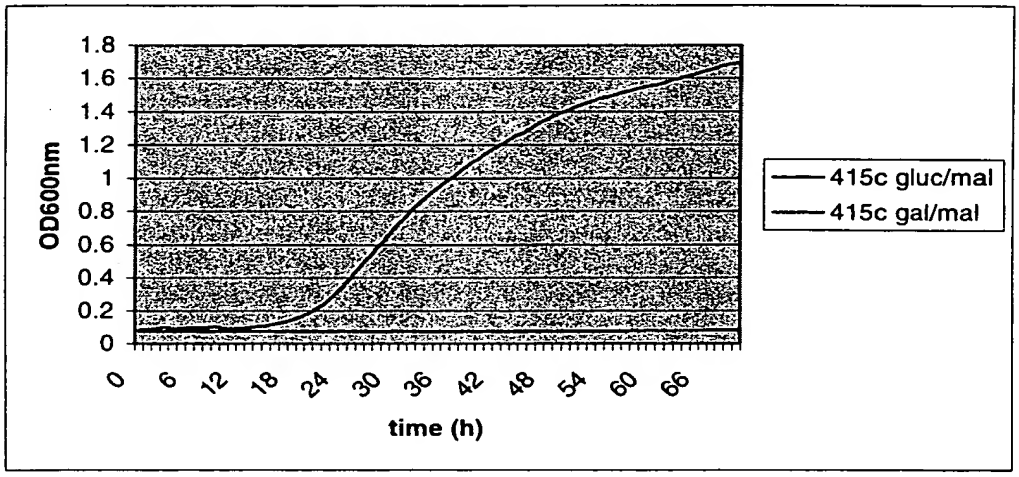

OD600nm
2
1.8
1.6
1.4
1.2
1
0.8
0.6
0.4
0.2
0
0
10
20
30
40
50
60
70
time (h)
38 gluc
38 gal

FIG. 3.





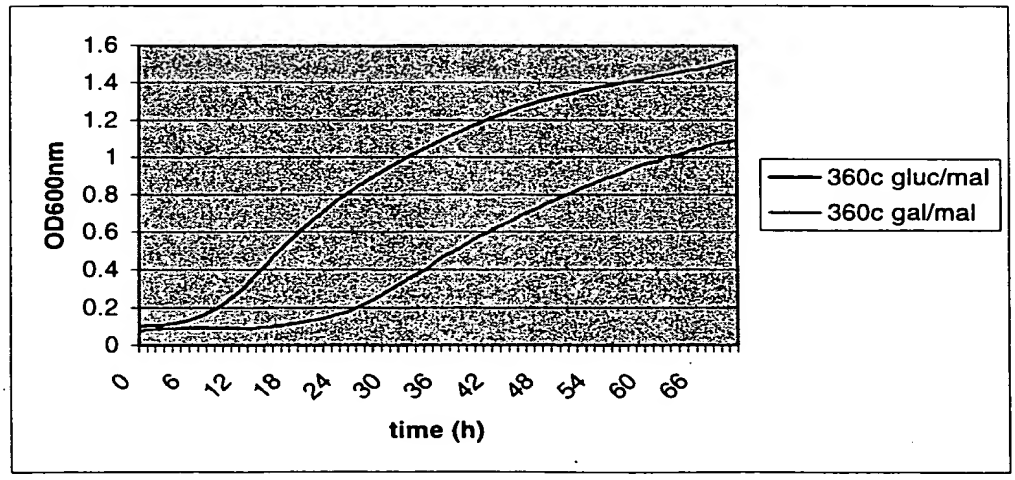


FIG. 3 (CONTINUED)

FIG. 4.

ß-galactosidase activity GAL1 promoter
conc. ß-gal/conc. prot. (U/mg)
0.006
0.005
0.004
0.003
0.002
0.001
0.000
conc ß-gal/conc. prot (U/mg)
clones
LAC4/pGAL1pNIST-1 glucose O
LAC4/pGAL1pNIST-1 glucose O
LAC4/pGAL1pNIST-1 galactose O
LAC4/pGAL1pNIST-1 galactose O
LAC4/pGAL1pNIST-1 glucose + maltose O
LAC4/pGAL1pNIST-1 glucose + maltose O
LAC4/pGAL1pNIST-1 galactose + maltose O
LAC4/pGAL1pNIST-1 galactose + maltose O
LAC4/pGAL1pNIST-1 glucose R
LAC4/pGAL1pNIST-1 glucose R
LAC4/pGAL1pNIST-1 galactose R
LAC4/pGAL1pNIST-1 galactose R
LAC4/pGAL1pNIST-1 glucose + maltose R
LAC4/pGAL1pNIST-1 glucose + maltose R
LAC4/pGAL1pNIST-1 galactose + maltose R
LAC4/pGAL1pNIST-1 galactose + maltose R
LAC4/pGAL1pNIST-1 glucose S
LAC4/pGAL1pNIST-1 glucose S
LAC4/pGAL1pNIST-1 galactose S
LAC4/pGAL1pNIST-1 galactose S
LAC4/pGAL1pNIST-1 glucose + maltose S
LAC4/pGAL1pNIST-1 glucose + maltose S
LAC4/pGAL1pNIST-1 galactose + maltose S
LAC4/pGAL1pNIST-1 galactose + maltose S
LAC4/pGAL1pNIST-1 glucose T
LAC4/pGAL1pNIST-1 glucose T
LAC4/pGAL1pNIST-1 galactose T
LAC4/pGAL1pNIST-1 galactose T
LAC4/pGAL1pNIST-1 glucose + maltose T
LAC4/pGAL1pNIST-1 glucose + maltose T
LAC4/pGAL1pNIST-1 galactose + maltose T
LAC4/pGAL1pNIST-1 galactose + maltose T

Figure 5:

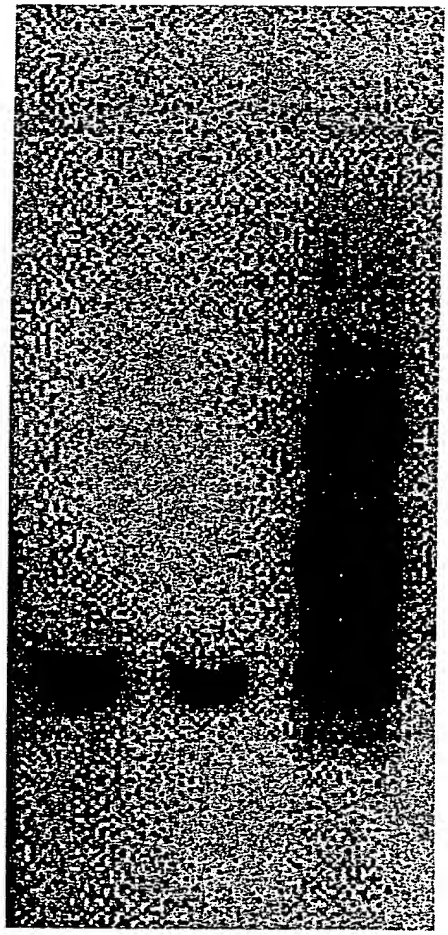
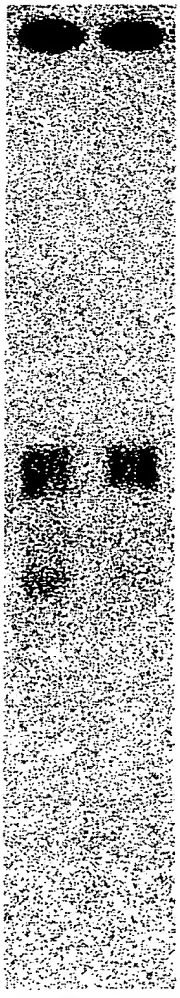
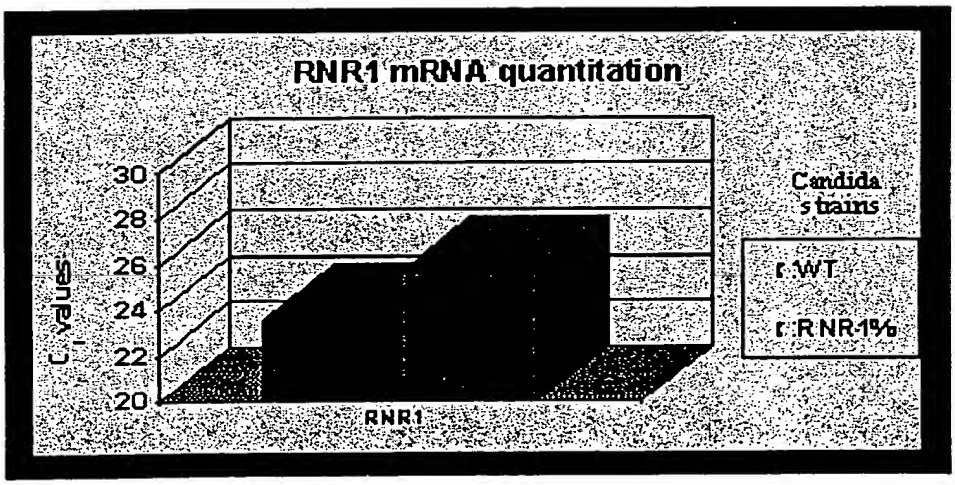


Figure 6A



1: RNR1 mutant
2: Wild type

Figure 6B


RNR1 mRNA quantitation
C_T plus
30
28
26
24
22
20
RNR1
Candida strains
r WT
r RNR1%

11/75 FIG. 7

HindIII

```
   1  AGCTTGAGTA TTCTATAGTG TCACCTAAAT AGCTTGGCGT AATCATGGTC
      TCGAACTCAT AAGATATCAC AGTGGATTTA TCGAACCGCA TTAGTACCAG

  51  ATAGCTGTTT CCTGTGTGAA ATTGTTATCC GCTCACAATT CCACACAACA
      TATCGACAAA GGACACACTT TAACAATAGG CGAGTGTTAA GGTGTGTTGT

 101  TACGAGCCGG AAGCATAAAG TGTAAAGCCT GGGGTGCCTA ATGAGTGAGC
      ATGCTCGGCC TTCGTATTTC ACATTTCGGA CCCCACGGAT TACTCACTCG

 151  TAACTCACAT TAATTGCGTT GCGCTCACTG CCCGCTTTCC AGTCGGGAAA
      ATTGAGTGTA ATTAACGCAA CGCGAGTGAC GGGCGAAAGG TCAGCCCTTT

 201  CCTGTCGTGC CAGCTGCATT AATGAATCGG CCAACGCGCG GGGAGAGGCG
      GGACAGCACG GTCGACGTAA TTACTTAGCC GGTTGCGCGC CCCTCTCCGC

 251  GTTTGCGTAT TGGGCGCTCT TCCGCTTCCT CGCTCACTGA CTCGCTGCGC
      CAAACGCATA ACCCGCGAGA AGGCGAAGGA GCGAGTGACT GAGCGACGCG

 301  TCGGTCGTTC GGCTGCGGCG AGCGGTATCA GCTCACTCAA AGGCGGTAAT
      AGCCAGCAAG CCGACGCCGC TCGCCATAGT CGAGTGAGTT TCCGCCATTA

 351  ACGGTTATCC ACAGAATCAG GGGATAACGC AGGAAAGAAC ATGTGAGCAA
      TGCCAATAGG TGTCTTAGTC CCCTATTGCG TCCTTTCTTG TACACTCGTT

 401  AAGGCCAGCA AAAGGCCAGG AACCGTAAAA AGGCCGCGTT GCTGGCGTTT
      TTCCGGTCGT TTTCCGGTCC TTGGCATTTT TCCGGCGCAA CGACCGCAAA

 451  TTCCATAGGC TCCGCCCCCC TGACGAGCAT CACAAAAATC GACGCTCAAG
      AAGGTATCCG AGGCGGGGGG ACTGCTCGTA GTGTTTTTAG CTGCGAGTTC

 501  TCAGAGGTGG CGAAACCCGA CAGGACTATA AAGATACCAG GCGTTTCCCC
      AGTCTCCACC GCTTTGGGCT GTCCTGATAT TTCTATGGTC CGCAAAGGGG

 551  CTGGAAGCTC CCTCGTGCGC TCTCCTGTTC CGACCCTGCC GCTTACCGGA
      GACCTTCGAG GGAGCACGCG AGAGGACAAG GCTGGGACGG CGAATGGCCT

 601  TACCTGTCCG CCTTTCTCCC TTCGGGAAGC GTGGCGCTTT CTCATAGCTC
      ATGGACAGGC GGAAAGAGGG AAGCCCTTCG CACCGCGAAA GAGTATCGAG

 651  ACGCTGTAGG TATCTCAGTT CGGTGTAGGT CGTTCGCTCC AAGCTGGGCT
      TGCGACATCC ATAGAGTCAA GCCACATCCA GCAAGCGAGG TTCGACCCGA
```

ApaLI

```
 701  GTGTGCACGA ACCCCCCGTT CAGCCCGACC GCTGCGCCTT ATCCGGTAAC
      CACACGTGCT TGGGGGGCAA GTCGGGCTGG CGACGCGGAA TAGGCCATTG

 751  TATCGTCTTG AGTCCAACCC GGTAAGACAC GACTTATCGC CACTGGCAGC
      ATAGCAGAAC TCAGGTTGGG CCATTCTGTG CTGAATAGCG GTGACCGTCG

 801  AGCCACTGGT AACAGGATTA GCAGAGCGAG GTATGTAGGC GGTGCTACAG
      TCGGTGACCA TTGTCCTAAT CGTCTCGCTC CATACATCCG CCACGATGTC

 851  AGTTCTTGAA GTGGTGGCCT AACTACGGCT ACACTAGAAG GACAGTATTT
      TCAAGAACTT CACCACCGGA TTGATGCCGA TGTGATCTTC CTGTCATAAA

 901  GGTATCTGCG CTCTGCTGAA GCCAGTTACC TTCGGAAAAA GAGTTGGTAG
      CCATAGACGC GAGACGACTT CGGTCAATGG AAGCCTTTTT CTCAACCATC
```

FIG. 7 (CONTINUED)

```
 951  CTCTTGATCC GGCAAACAAA CCACCGCTGG TAGCGGTGGT TTTTTTGTTT
      GAGAACTAGG CCGTTTGTTT GGTGGCGACC ATCGCCACCA AAAAAACAAA
 .....

1001  GCAAGCAGCA GATTACGCGC AGAAAAAAAG GATCTCAAGA AGATCCTTTG
      CGTTCGTCGT CTAATGCGCG TCTTTTTTTC CTAGAGTTCT TCTAGGAAAC
 .....

1051  ATCTTTTCTA CGGGGTCTGA CGCTCAGTGG AACGAAAACT CACGTTAAGG
      TAGAAAAGAT GCCCCAGACT GCGAGTCACC TTGCTTTTGA GTGCAATTCC
 .....

1101  GATTTTGGTC ATGAGATTAT CAAAAAGGAT CTTCACCTAG ATCCTTTTAA
      CTAAAACCAG TACTCTAATA GTTTTTCCTA GAAGTGGATC TAGGAAAATT
 .....

1151  ATTAAAAATG AAGTTTTAAA TCAATCTAAA GTATATATGA GTAAACTTGG
      TAATTTTTAC TTCAAAATTT AGTTAGATTT CATATATACT CATTTGAACC
 .....

1201  TCTGACAGTT ACCAATGCTT AATCAGTGAG GCACCTATCT CAGCGATCTG
      AGACTGTCAA TGGTTACGAA TTAGTCACTC CGTGGATAGA GTCGCTAGAC
 .....

1251  TCTATTTCGT TCATCCATAG TTGCCTGACT CCCCGTCGTG TAGATAACTA
      AGATAAAGCA AGTAGGTATC AACGGACTGA GGGGCAGCAC ATCTATTGAT
 .....

1301  CGATACGGGA GGGCTTACCA TCTGGCCCCA GTGCTGCAAT GATACCGCGA
      GCTATGCCCT CCCGAATGGT AGACCGGGGT CACGACGTTA CTATGGCGCT
 .....

1351  GACCCACGCT CACCGGCTCC AGATTTATCA GCAATAAACC AGCCAGCCGG
      CTGGGTGCGA GTGGCCGAGG TCTAAATAGT CGTTATTTGG TCGGTCGGCC
 .....

1401  AAGGGCCGAG CGCAGAAGTG GTCCTGCAAC TTTATCCGCC TCCATCCAGT
      TTCCCGGCTC GCGTCTTCAC CAGGACGTTG AAATAGGCGG AGGTAGGTCA
 .....

1451  CTATTAATTG TTGCCGGGAA GCTAGAGTAA GTAGTTCGCC AGTTAATAGT
      GATAATTAAC AACGGCCCTT CGATCTCATT CATCAAGCGG TCAATTATCA
 .....

1501  TTGCGCAACG TTGTTGCCAT TGCTACAGGC ATCGTGGTGT CACGCTCGTC
      AACGCGTTGC AACAACGGTA ACGATGTCCG TAGCACCACA GTGCGAGCAG
 .....

1551  GTTTGGTATG GCTTCATTCA GCTCCGGTTC CCAACGATCA AGGCGAGTTA
      CAAACCATAC CGAAGTAAGT CGAGGCCAAG GGTTGCTAGT TCCGCTCAAT
 .....

1601  CATGATCCCC CATGTTGTGC AAAAAAGCGG TTAGCTCCTT CGGTCCTCCG
      GTACTAGGGG GTACAACACG TTTTTTCGCC AATCGAGGAA GCCAGGAGGC
 .....

1651  ATCGTTGTCA GAAGTAAGTT GGCCGCAGTG TTATCACTCA TGGTTATGGC
      TAGCAACAGT CTTCATTCAA CCGGCGTCAC AATAGTGAGT ACCAATACCG
 .....

1701  AGCACTGCAT AATTCTCTTA CTGTCATGCC ATCCGTAAGA TGCTTTTCTG
      TCGTGACGTA TTAAGAGAAT GACAGTACGG TAGGCATTCT ACGAAAAGAC
 .....

1751  TGACTGGTGA GTACTCAACC AAGTCATTCT GAGAATAGTG TATGCGGCGA
      ACTGACCACT CATGAGTTGG TTCAGTAAGA CTCTTATCAC ATACGCCGCT
 .....

1801  CCGAGTTGCT CTTGCCCGGC GTCAATACGG GATAATACCG CGCCACATAG
      GGCTCAACGA GAACGGGCCG CAGTTATGCC CTATTATGGC GCGGTGTATC
 .....

1851  CAGAACTTTA AAAGTGCTCA TCATTGGAAA ACGTTCTTCG GGGCGAAAAC
      GTCTTGAAAT TTTCACGAGT AGTAACCTTT TGCAAGAAGC CCCGCTTTTG
 .....
```

FIG. 7. (CONTINUED)

```
                                                                ApaLI
                                                                --
1901  TCTCAAGGAT CTTACCGCTG TTGAGATCCA GTTCGATGTA ACCCACTCGT
      AGAGTTCCTA GAATGGCGAC AACTCTAGGT CAAGCTACAT TGGGTGAGCA
 .....

      ApaLI
      ----
1951  GCACCCAACT GATCTTCAGC ATCTTTTACT TTCACCAGCG TTTCTGGGTG
      CGTGGGTTGA CTAGAAGTCG TAGAAAATGA AAGTGGTCGC AAAGACCCAC
 .....

2001  AGCAAAAACA GGAAGGCAAA ATGCCGCAAA AAAGGGAATA AGGGCGACAC
      TCGTTTTTGT CCTTCCGTTT TACGGCGTTT TTTCCCTTAT TCCCGCTGTG
 .....

2051  GGAAATGTTG AATACTCATA CTCTTCCTTT TTCAATATTA TTGAAGCATT
      CCTTTACAAC TTATGAGTAT GAGAAGGAAA AAGTTATAAT AACTTCGTAA
 .....

2101  TATCAGGGTT ATTGTCTCAT GAGCGGATAC ATATTTGAAT GTATTTAGAA
      ATAGTCCCAA TAACAGAGTA CTCGCCTATG TATAAACTTA CATAAATCTT
 .....

2151  AAATAAACAA ATAGGGGTTC CGCGCACATT TCCCCGAAAA GTGCCACCTG
      TTTATTTGTT TATCCCCAAG GCGCGTGTAA AGGGGCTTTT CACGGTGGAC
 .....

2201  ACGTCTAAGA AACCATTATT ATCATGACAT TAACCTATAA AAATAGGCGT
      TGCAGATTCT TTGGTAATAA TAGTACTGTA ATTGGATATT TTTATCCGCA
 .....

2251  ATCACGAGGC CCTTTCGTCT CGCGCGTTTC GGTGATGACG GTGAAAACCT
      TAGTGCTCCG GGAAAGCAGA GCGCGCAAAG CCACTACTGC CACTTTTGGA
 .....

2301  CTGACACATG CAGCTCCCGG AGACGGTCAC AGCTTGTCTG TAAGCGGATG
      GACTGTGTAC GTCGAGGGCC TCTGCCAGTG TCGAACAGAC ATTCGCCTAC
 .....

2351  CCGGGAGCAG ACAAGCCCGT CAGGGCGCGT CAGCGGGTGT TGGCGGGTGT
      GGCCCTCGTC TGTTCGGGCA GTCCCGCGCA GTCGCCCACA ACCGCCCACA
 .....

                                                          ApaLI
                                                          -----
2401  CGGGGCTGGC TTAACTATGC GGCATCAGAG CAGATTGTAC TGAGAGTGCA
      GCCCCGACCG AATTGATACG CCGTAGTCTC GTCTAACATG ACTCTCACGT
 .....

      ApaLI
      -
2451  CCATATGCGG TGTGAAATAC CGCACAGATG CGTAAGGAGA AAATACCGCA
      GGTATACGCC ACACTTTATG GCGTGTCTAC GCATTCCTCT TTTATGGCGT
 .....

2501  TCAGGCGAAA TTGTAAACGT TAATATTTTG TTAAAATTCG CGTTAAATAT
      AGTCCGCTTT AACATTTGCA ATTATAAAAC AATTTTAAGC GCAATTTATA
 .....

2551  TTGTTAAATC AGCTCATTTT TTAACCAATA GGCCGAAATC GGCAAAATCC
      AACAATTTAG TCGAGTAAAA AATTGGTTAT CCGGCTTTAG CCGTTTTAGG
 .....

2601  CTTATAAATC AAAAGAATAG ACCGAGATAG GGTTGAGTGT TGTTCCAGTT
      GAATATTTAG TTTTCTTATC TGGCTCTATC CCAACTCACA ACAAGGTCAA
 .....

2651  TGGAACAAGA GTCCACTATT AAAGAACGTG GACTCCAACG TCAAAGGGCG
      ACCTTGTTCT CAGGTGATAA TTTCTTGCAC CTGAGGTTGC AGTTTCCCGC
 .....

2701  AAAAACCGTC TATCAGGGCG ATGGCCCACT ACGTGAACCA TCACCCAAAT
      TTTTTGGCAG ATAGTCCCGC TACCGGGTGA TGCACTTGGT AGTGGGTTTA
 .....

2751  CAAGTTTTTT GCGGTCGAGG TGCCGTAAAG CTCTAAATCG GAACCCTAAA
      GTTCAAAAAA CGCCAGCTCC ACGGCATTTC GAGATTTAGC CTTGGGATTT
 .....
```

FIG. 7 (CONTINUED)

```
2801  GGGAGCCCCC GATTTAGAGC TTGACGGGGA AAGCCGGCGA ACGTGGCGAG
      CCCTCGGGGG CTAAATCTCG AACTGCCCCT TTCGGCCGCT TGCACCGCTC
.....
2851  AAAGGAAGGG AAGAAAGCGA AAGGAGCGGG CGCTAGGGCG CTGGCAAGTG
      TTTCCTTCCC TTCTTTCGCT TTCCTCGCCC GCGATCCCGC GACCGTTCAC
.....
2901  TAGCGGTCAC GCTGCGCGTA ACCACCACAC CCGCCGCGCT TAATGCGCCG
      ATCGCCAGTG CGACGCGCAT TGGTGGTGTG GGCGGCGCGA ATTACGCGGC
.....
2951  CTACAGGGCG CGTCCATTCG CCATTCAGGC TGCGCAACTG TTGGGAAGGG
      GATGTCCCGC GCAGGTAAGC GGTAAGTCCG ACGCGTTGAC AACCCTTCCC
.....
3001  CGATCGGTGC GGGCCTCTTC GCTATTACGC CAGCTGGCGA AAGGGGGATG
      GCTAGCCACG CCCGGAGAAG CGATAATGCG GTCGACCGCT TTCCCCCTAC
.....
3051  TGCTGCAAGG CGATTAAGTT GGGTAACGCC AGGGTTTTCC CAGTCACGAC
      ACGACGTTCC GCTAATTCAA CCCATTGCGG TCCCAAAAGG GTCAGTGCTG
.....
3101  GTTGTAAAAC GACGGCCAGT GAATTGTAAT ACGACTCACT ATAGGGCGAA
      CAACATTTTG CTGCCGGTCA CTTAACATTA TGCTGAGTGA TATCCCGCTT
.....
3151  TTGGTTTTCC AATGATGAGC ACTTTTAAAG TTCTGCTATG TGGCGCGGTA
      AACCAAAAGG TTACTACTCG TGAAAATTTC AAGACGATAC ACCGCGCCAT
.....
3201  TTATCCCGTG TTGACGCCGG GCAAGAGCAA CTCGGTCGCC GCATACACTA
      AATAGGGCAC AACTGCGGCC CGTTCTCGTT GAGCCAGCGG CGTATGTGAT
.....
3251  TTCTCAGAAT GACTTGGTTG AGTACTAATA GGAATTGATT TGGATGGTAT
      AAGAGTCTTA CTGAACCAAC TCATGATTAT CCTTAACTAA ACCTACCATA
.....
3301  AAACGGAAAC AAAAAAAAGA GCTGGTACTA CTTTCTTTAA AATTATTTTA
      TTTGCCTTTG TTTTTTTTCT CGACCATGAT GAAAGAAATT TTAATAAAAT
.....
3351  TTATTTGATT TTATTTAATA GTATATATTA TATTTTGAAC GTAGATTATT
      AATAAACTAA AATAAATTAT CATATATAAT ATAAAACTTG CATCTAATAA
.....
3401  TTGTTGAAAG TTGCTGTAGT GCCATTGATT CGTAACACTA ATTCTGTATT
      AACAACTTTC AACGACATCA CGGTAACTAA GCATTGTGAT TAAGACATAA
.....
3451  AGTCATTCCT CTTGTTTGAT AGTATCCAAA AAAACGGCTA TTTTTTTGCA
      TCAGTAAGGA GAACAAACTA TCATAGGTTT TTTTGCCGAT AAAAAAACGT
.....
3501  ATCTTATTTC CTGCATATTA TACAGATAAC ATAATGAAAG AAAAAATCTT
      TAGAATAAAG GACGTATAAT ATGTCTATTG TATTACTTTC TTTTTTAGAA
.....
3551  TTTTTTTGTT CTTCAATGAT GATTTCAACC ATTCTTTTAA ACATTGATCA
      AAAAAAACAA GAAGTTACTA CTAAAGTTGG TAAGAAAATT TGTAACTAGT
.....
3601  ATTCCTGAGC AACAACCCCA TACACACTGG TTTATATACC GCCCCTTTTA
      TAAGGACTCG TTGTTGGGGT ATGTGTGACC AAATATATGG CGGGGAAAAT
.....
3651  CAGTTGAAGA AAGAAATAGA AATAGAAATA GCAAACAAAA GATATGACAG
      GTCAACTTCT TTCTTTATCT TTATCTTTAT CGTTTGTTTT CTATACTGTC
.....
3701  TCAACACTAA GACCTATAGT GAGAGAGCAG AAACTCATGC CTCACCAGTA
      AGTTGTGATT CTGGATATCA CTCTCTCGTC TTTGAGTACG GAGTGGTCAT
.....
3751  GCACAGCGAT TATTTCGATT AATGGAACTG AAGAAAACCA ATTTATGTGC
      CGTGTCGCTA ATAAAGCTAA TTACCTTGAC TTCTTTTGGT TAAATACACG
.....
```

FIG. 7. (CONTINUED)

EcoRI

```
3801  ATCAATTGAC GTTGATACCA CTAAGGAATT CCTTGAATTA ATTGATAAAT
      TAGTTAACTG CAACTATGGT GATTCCTTAA GGAACTTAAT TAACTATTTA

3851  TAGGTCCTTA TGTATGCTTA ATCAAGACTC ATATTGATAT AATCAATGAT
      ATCCAGGAAT ACATACGAAT TAGTTCTGAG TATAACTATA TTAGTTACTA

3901  TTTTCCTATG AATCCACTAT TGAACCATTA TTAGAACTTT CACGTAAACA
      AAAAGGATAC TTAGGTGATA ACTTGGTAAT AATCTTGAAA GTGCATTTGT

3951  TCAATTTATG ATTTTTGAAG ATAGAAAATT TGCTGATATT GGTAATACCG
      AGTTAAATAC TAAAAACTTC TATCTTTTAA ACGACTATAA CCATTATGGC

4001  TAAAGAAACA ATATATTGGT GGAGTTTATA AAATTAGTAG TTGGGCAGAT
      ATTTCTTTGT TATATAACCA CCTCAAATAT TTTAATCATC AACCCGTCTA

4051  ATTACCAATG CTCATGGTGT CACTGGGAAT GGAGTGGTTG AAGGATTAAA
      TAATGGTTAC GAGTACCACA GTGACCCTTA CCTCACCAAC TTCCTAATTT

4101  ACAGGGAGCT AAAGAAACCA CCACCAACCA AGAGCCAAGA GGGTTATTGA
      TGTCCCTCGA TTTCTTTGGT GGTGGTTGGT TCTCGGTTCT CCCAATAACT

4151  TGTTAGCTGA ATTATCATCA GTGGGATCAT TAGCATATGG AGAATATTCT
      ACAATCGACT TAATAGTAGT CACCCTAGTA ATCGTATACC TCTTATAAGA

4201  CAAAAAACTG TTGAAATTGC TAAATCCGAT AAGGAATTTG TTATTGGATT
      GTTTTTTGAC AACTTTAACG ATTTAGGCTA TTCCTTAAAC AATAACCTAA

4251  TATTGCCCAA CGTGATATGG GTGGCCAAGA AGAAGGATTT GATTGGCTTA
      ATAACGGGTT GCACTATACC CACCGGTTCT TCTTCCTAAA CTAACCGAAT

4301  TTATGACACC TGGAGTTGGA TTAGATGATA AAGGTGATGG ATTAGGACAA
      AATACTGTGG ACCTCAACCT AATCTACTAT TTCCACTACC TAATCCTGTT

4351  CAATATAGAA CTGTTGATGA AGTTGTTAGC ACTGGAACTG ATATTATCAT
      GTTATATCTT GACAACTACT TCAACAATCG TGACCTTGAC TATAATAGTA

4401  TGTTGGTAGA GGATTGTTTG GTAAAGGAAG AGATCCAGAT ATTGAAGGTA
      ACAACCATCT CCTAACAAAC CATTTCCTTC TCTAGGTCTA TAACTTCCAT

4451  AAAGGTATAG AAATGCTGGT TGGAATGCTT ATTTGAAAAA GACTGGCCAA
      TTTCCATATC TTTACGACCA ACCTTACGAA TAAACTTTTT CTGACCGGTT

4501  TTATAAATGT GAAGGGGGAG ATTTTCACTT TATTAGATTT GTATATATGT
      AATATTTACA CTTCCCCCTC TAAAAGTGAA ATAATCTAAA CATATATACA

4551  AGAATAAATA AATAAATAAG TTAAATAAAT AATTAAATAA GGGTGGTAAT
      TCTTATTTAT TTATTTATTC AATTTATTTA TTAATTTATT CCCACCATTA

4601  TATTACTATT TACAATCAAA GGTGGTCCTT CTAGCTGTAA TCCGGGCAGC
      ATAATGATAA ATGTTAGTTT CCACCAGGAA GATCGACATT AGGCCCGTCG

4651  GCAACGGAAC ATTCATCAGT GTAAAAATGG AATCAATAAA GCCCTGCGCA
      CGTTGCCTTG TAAGTAGTCA CATTTTTACC TTAGTTATTT CGGGACGCGT

4701  GCGCGCAGGG TCAGCCTGAA TACGCGTTTA ATGACCAGCA CAGTCGTGAT
      CGCGCGTCCC AGTCGGACTT ATGCGCAAAT TACTGGTCGT GTCAGCACTA
```

FIG. 7 (CONTINUED)

```
4751  GGCAAGGTCA GAATAGCCCA AGTCGGCCGA GGGGCCTGTA CAGTGAGGGA
      CCGTTCCAGT CTTATCGGGT TCAGCCGGCT CCCCGGACAT GTCACTCCCT
.....
4801  AGATCTGATA TTGACGAAGA GGAACCAATG TAACGTTACA CTGAAGAAAA
      TCTAGACTAT AACTGCTTCT CCTTGGTTAC ATTGCAATGT GACTTCTTTT
.....
4851  CACACAATAA ACGGGAAGAA ACGGTGTAAA AGTGTGAAAA TAATTTTTGA
      GTGTGTTATT TGCCCTTCTT TGCCACATTT TCACACTTTT ATTAAAAACT
.....
4901  ATATCATTTC CCTTGGTTTA ATTCCAAACG AAACGTGTTT TTTTTAGAGA
      TATAGTAAAG GGAACCAAAT TAAGGTTTGC TTTGCACAAA AAAAATCTCT
.....
          EcoRI                                          ApaLI
          ------                                         -----
4951  ATGGGAATTC TTATTGGATG TCTAGATTGT TTGTTTACTC CAGACTGTGC
      TACCCTTAAG AATAACCTAC AGATCTAACA AACAAATGAG GTCTGACACG
.....
      ApaLI
      --
5001  ACAAAAACGT TTGGATGGAT GATCAGAAGA TATTTTTAGG CTTAGCTCTA
      TGTTTTTGCA AACCTACCTA CTAGTCTTCT ATAAAAATCC GAATCGAGAT
.....
5051  AATATAAGAA ATGATGCTTG AAAAACCAGA CAGAAATTGA GTTTCAAAAA
      TTATATTCTT TACTACGAAC TTTTTGGTCT GTCTTTAACT CAAAGTTTTT
.....
5101  TTGGTAATGT GAGGTATTAG TCAACTAACC AAATAACAAT GCAAACCGGT
      AACCATTACA CTCCATAATC AGTTGATTGG TTTATTGTTA CGTTTGGCCA
.....
5151  TGATACATTT CATTTTGAAA ATAATGAAAC TGGAATTGGA TGACCAGCAC
      ACTATGTAAA GTAAAACTTT TATTACTTTG ACCTTAACCT ACTGGTCGTG
.....
5201  ACAAACACAT AAAGTAATTA TGGGAATTAG AAGCGAACAT AGAGGAGTAC
      TGTTTGTGTA TTTCATTAAT ACCCTTAATC TTCGCTTGTA TCTCCTCATG
.....
5251  TTGGCCACGA ACAGAATACA AGTGGGAACA CTATTTTCTC CATTGTTTTA
      AACCGGTGCT TGTCTTATGT TCACCCTTGT GATAAAAGAG GTAACAAAAT
.....
5301  GTTCTGTTTT TTTGTCAGCC TAGTTTTGTG CTATGTGTAA AAAATATTGC
      CAAGACAAAA AAACAGTCGG ATCAAAACAC GATACACATT TTTTATAACG
.....
              HindIII
              -------
5351  CAAGAAAAAA AGCTTGTTTT GTGGCCAGTG TCCGAAAAAA ATTTTGGGGA
      GTTCTTTTTT TCGAACAAAA CACCGGTCAC AGGCTTTTTT TAAAACCCCT
.....
5401  ATCTTCGGAT TAATTTATGT TTTCATTCCA TCGGGGAAAG TGGGGGGGAA
      TAGAAGCCTA ATTAAATACA AAAGTAAGGT AGCCCCTTTC ACCCCCCCTT
.....
5451  AAAATTTTAA GCAGTTCACA AAACCTTCCA AAAAATATAT GGACAAAGAT
      TTTTAAAATT CGTCAAGTGT TTTGGAAGGT TTTTTATATA CCTGTTTCTA
.....
5501  GATTGTATTT TCCCGACACC AAAATCATAA TTAATTATGA GAAAGTTAAA
      CTAACATAAA AGGGCTGTGG TTTTAGTATT AATTAATACT CTTTCAATTT
.....
5551  TGTAACGTTA CAATTTATGT TTATTTGAAG GTGAAAAGCG ATTTATGATT
      ACATTGCAAT GTTAAATACA AATAAACTTC CACTTTTCGC TAAATACTAA
.....
5601  TTTCCGAAAT GAAAATTTTT TTTAGGTTTA TTTTTTTTGT CGGGCAAAGA
      AAAGGCTTTA CTTTTAAAAA AAATCCAAAT AAAAAAAACA GCCCGTTTCT
.....
```

FIG. 7. (CONTINUED)

EcoRI

```
5651  AAAACTGAAC AAGGATTATT AAAATTTTTG GTGTTTGTTT GTGTCTGGAG
      TTTTGACTTG TTCCTAATAA TTTTAAAAAC CACAAACAAA CACAGACCTC
```

EcoRI

```
5701  AATTCATTCC TCTCTCATCT TCACACAATG TTTAGACATC TGACACGATT
      TTAAGTAAGG AGAGAGTAGA AGTGTGTTAC AAATCTGTAG ACTGTGCTAA
```

```
5751  CATGATAGTT CGGTTTCCGG GGTTGGTGTT TAGTTTTCGT TTTTCTTTTT
      GTACTATCAA GCCAAAGGCC CCAACCACAA ATCAAAAGCA AAAAGAAAAA
```

```
5801  TTTTGGAAAG AATGTTTTAG CTCATTGGTT TTCTTTCTTC ATTCAATAGT
      AAAACCTTTC TTACAAAATC GAGTAACCAA AAGAAAGAAG TAAGTTATCA
```

```
5851  TTTGAAAGAA TTTGCCCACT TGTTATTACA ATCATATAAA ATTAAACTTT
      AAACTTTCTT AAACGGGTGA ACAATAATGT TAGTATATTT TAATTTGAAA
```

```
5901  GATATAAAAT AGAGTTTGAA AGTTTCCCAG ATCCTTTTTG ATTTCTTTGT
      CTATATTTTA TCTCAAACTT TCAAAGGGTC TAGGAAAAAC TAAAGAAACA
```

```
5951  AAATTTTTTT TTCTCCCACA TATACACACA TACAAACCGA TTTTTATAAG
      TTTAAAAAAA AAGAGGGTGT ATATGTGTGT ATGTTTGGCT AAAAATATTC
```

PstI AvaI BamHI

```
6001  AAAGAGTTAT ACCCTGCAGC TCGACCTCGA GGGATCCGGG CCCTCTAGAT
      TTTCTCAATA TGGGACGTCG AGCTGGAGCT CCCTAGGCCC GGGAGATCTA
```

AvaI

```
6051  GCGGCCGCTA GGCCTCGAGG GACTTTTGCA CCAAAAATAA TTTATTTTCC
      CGCCGGCGAT CCGGAGCTCC CTGAAAACGT GGTTTTTATT AAATAAAAGG
```

```
6101  AAAATAAAAT TTAAATAAAT AAAAATAACT CATAATTTAA TAAAAATTTC
      TTTTATTTTA AATTTATTTA TTTTTATTGA GTATTAAATT ATTTTTAAAG
```

```
6151  AAAATCTTCT AGTGTCCTTT CATATGCAGT ACATTAGCCA TCAGTCACTT
      TTTTAGAAGA TCACAGGAAA GTATACGTCA TGTAATCGGT AGTCAGTGAA
```

```
6201  AAACAGCATC TGCTGGTTGA AGAATGCTTG AAGCAATTGT CCAGTCCCAG
      TTTGTCGTAG ACGACCAACT TCTTACGAAC TTCGTTAACA GGTCAGGGTC
```

```
6251  AGGCACAGGC TAGGAGATCT TCAGTTTCGG AGGTAACCTG TAAGTCTGTT
      TCCGTGTCCG ATCCTCTAGA AGTCAAAGCC TCCATTGGAC ATTCAGACAA
```

```
6301  AATGAAGTAA AAGTTCCTTA GGATTTCCAC TCTGACTATG GTCCAGGCAC
      TTACTTCATT TTCAAGGAAT CCTAAAGGTG AGACTGATAC CAGGTCCGTG
```

```
6351  AGTGACTGTA CTCCTTGGCC TTCAGGTAAT GCAGAATCCT CCCATAATAT
      TCACTGACAT GAGGAACCGG AAGTCCATTA CGTCTTAGGA GGGTATTATA
```

```
6401  CTTTTCAGGT GCAGACTGCT CATGAGTTTT CCCCTGGTGA AATCTTCTTT
      GAAAAGTCCA CGTCTGACGA GTACTCAAAA GGGGACCACT TTAGAAGAAA
```

```
6451  CTCCAGTTTT TCTTCCAGGA CTGTCTTCAG ATGGTTTATC TGATGATAGA
      GAGGTCAAAA AGAAGGTCCT GACAGAAGTC TACCAAATAG ACTACTATCT
```

```
6501  CATTAGCCAG GAGGTTCTCA ACAATAGTCT CATTCCAGCC AGTGCTAGAT
      GTAATCGGTC CTCCAAGAGT TGTTATCAGA GTAAGGTCGG TCACGATCTA
```

FIG. 7. (CONTINUED)

```
6551  GAATCTTGTC TGAAAATAGC AAAGATGTTC TGGAGCATCT CATAGATGGT
      CTTAGAACAG ACTTTTATCG TTTCTACAAG ACCTCGTAGA GTATCTACCA
 .....

                                    PstI
                                    -------
6601  CAATGCGGCG TCCTCCTTCT GGAACTGCTG CAGCTGCTTA ATCTCCTCAG
      GTTACGCCGC AGGAGGAAGA CCTTGACGAC GTCGACGAAT TAGAGGAGTC
 .....

6651  GGATGTCAAA GTTCATCCTG TCCTTGAGGC AGTATTCAAG CCTCCCATTC
      CCTACAGTTT CAAGTAGGAC AGGAACTCCG TCATAAGTTC GGAGGGTAAG
 .....

6701  AATTGCCACA GGAGCTTCTG ACACTGAAAA TTGCTGCTTC TTTGTAGGAA
      TTAACGGTGT CCTCGAAGAC TGTGACTTTT AACGACGAAG AAACATCCTT
 .....

6751  TCCAAGCAAG TTGTAGCTCA TGGAAAGAGC TGTAGTGGAG AAGCACAACA
      AGGTTCGTTC AACATCGAGT ACCTTTCTCG ACATCACCTC TTCGTGTTGT
 .....

                                              AvaI
                                              -------
6801  GGAGAGCAAT TTGGAGGAGA CACTTGTTGG TCATGTTCCT CGAGGCCTTT
      CCTCTCGTTA AACCTCCTCT GTGAACAACC AGTACAAGGA GCTCCGGAAA
 .....

                                                    BamHI
                                                    ---
6851  TTGGCCAGCT GGCGCCTGCT GCGCGACGGC GAGCTGCTCA CCACCCAGGA
      AACCGGTCGA CCGCGGACGA CGCGCTGCCG CTCGACGAGT GGTGGGTCCT
 .....

      BamHI
      ---
6901  TCCGTCCCCC TTTTCCTTTG TCGATATCAT GTAATTAGTT ATGTCACGCT
      AGGCAGGGGG AAAAGGAAAC AGCTATAGTA CATTAATCAA TACAGTGCGA
 .....

6951  TACATTCACG CCCTCCCCCC ACATCCGCTC TAACCGAAAA GGAAGGAGTT
      ATGTAAGTGC GGGAGGGGGG TGTAGGCGAG ATTGGCTTTT CCTTCCTCAA
 .....

7001  AGACAACCTG AAGTCTAGGT CCCTATTTAT TTTTTTATAG TTATGTTAGT
      TCTGTTGGAC TTCAGATCCA GGGATAAATA AAAAAATATC AATACAATCA
 .....

7051  ATTAAGAACG TTATTTATAT TTCAAATTTT TCTTTTTTTT CTGTACAGAC
      TAATTCTTGC AATAAATATA AAGTTTAAAA AGAAAAAAAA GACATGTCTG
 .....

7101  GCGTGTACGC ATGTAACATT ATACTGAAAA CCTTGCTTGA GAAGGTTTTG
      CGCACATGCG TACATTGTAA TATGACTTTT GGAACGAACT CTTCCAAAAC
 .....

                        HindIII
                        -
7151  GGACGCTCGA AGGCTTTAAT TTGCA
      CCTGCGAGCT TCCGAAATTA AACGT
 .....
```

FIG. 8.

```
   1  TTCCATCGGG GAAAGTGGGG GGGAAAAAAT TTTAAGCAGT TCACAAAACC
      AAGGTAGCCC CTTTCACCCC CCCTTTTTTA AAATTCGTCA AGTGTTTTGG
 .....
  51  TTCCAAAAAA TATATGGACA AAGATGATTG TATTTTCCCG ACACCAAAAT
      AAGGTTTTTT ATATACCTGT TTCTACTAAC ATAAAAGGGC TGTGGTTTTA
 .....
 101  CATAATTAAT TATGAGAAAG TTAAATGTAA CGTTACAATT TATGTTTATT
      GTATTAATTA ATACTCTTTC AATTTACATT GCAATGTTAA ATACAAATAA
 .....
 151  TGAAGGTGAA AAGCGATTTA TGATTTTTCC GAAATGAAAA TTTTTTTTAG
      ACTTCCACTT TTCGCTAAAT ACTAAAAAGG CTTTACTTTT AAAAAAAATC
 .....
 201  GTTTATTTTT TTTGTCGGGC AAAGAAAAAC TGAACAAGGA TTATTAAAAT
      CAAATAAAAA AAACAGCCCG TTTCTTTTTG ACTTGTTCCT AATAATTTTA
 .....
                                EcoRI
                                ------
 251  TTTTGGTGTT TGTTTGTGTC TGGAGAATTC ATTCCTCTCT CATCTTCACA
      AAAACCACAA ACAAACACAG ACCTCTTAAG TAAGGAGAGA GTAGAAGTGT
 .....
 301  CAATGTTTAG ACATCTGACA CGATTCATGA TAGTTCGGTT TCCGGGGTTG
      GTTACAAATC TGTAGACTGT GCTAAGTACT ATCAAGCCAA AGGCCCCAAC
 .....
 351  GTGTTTAGTT TTCGTTTTTC TTTTTTTTTG GAAAGAATGT TTTAGCTCAT
      CACAAATCAA AAGCAAAAAG AAAAAAAAAC CTTTCTTACA AAATCGAGTA
 .....
 401  TGGTTTTCTT TCTTCATTCA ATAGTTTTGA AAGAATTTGC CCACTTGTTA
      ACCAAAAGAA AGAAGTAAGT TATCAAAACT TTCTTAAACG GGTGAACAAT
 .....
 451  TTACAATCAT ATAAAATTAA ACTTTGATAT AAAATAGAGT TTGAAAGTTT
      AATGTTAGTA TATTTTAATT TGAAACTATA TTTTATCTCA AACTTTCAAA
 .....
 501  CCCAGATCCT TTTTGATTTC TTTGTAAATT TTTTTTTCTC CCACATATAC
      GGGTCTAGGA AAAACTAAAG AAACATTTAA AAAAAAAGAG GGTGTATATG
 .....
                                                  PstI
                                                  -------
 551  ACACATACAA ACCGATTTTT ATAAGAAAGA GTTATACCCT GCAGCTCGAC
      TGTGTATGTT TGGCTAAAAA TATTCTTTCT CAATATGGGA CGTCGAGCTG
 .....
                      PstI          HindIII              AvaI
                      -------       -------              -----
 601  CTCGACTGTT TAAACCTGCA GGCATGCAAG CTTGGCCAAA AAGGCCTCGA
      GAGCTGACAA ATTTGGACGT CCGTACGTTC GAACCGGTTT TTCCGGAGCT
 .....
      AvaI
      -
 651  GGAACATGAC CAACAAGTGT CTCCTCCAAA TTGCTCTCCT GTTGTGCTTC
      CCTTGTACTG GTTGTTCACA GAGGAGGTTT AACGAGAGGA CAACACGAAG
 .....
 701  TCCACTACAG CTCTTTCCAT GAGCTACAAC TTGCTTGGAT TCCTACAAAG
      AGGTGATGTC GAGAAAGGTA CTCGATGTTG AACGAACCTA AGGATGTTTC
 .....
 751  AAGCAGCAAT TTTCAGTGTC AGAAGCTCCT GTGGCAATTG AATGGGAGGC
      TTCGTCGTTA AAAGTCACAG TCTTCGAGGA CACCGTTAAC TTACCCTCCG
 .....
 801  TTGAATACTG CCTCAAGGAC AGGATGAACT TTGACATCCC TGAGGAGATT
      AACTTATGAC GGAGTTCCTG TCCTACTTGA AACTGTAGGG ACTCCTCTAA
 .....
```

FIG. 8. (CONTINUED)

```
            PstI
            -------
 851  AAGCAGCTGC AGCAGTTCCA GAAGGAGGAC GCCGCATTGA CCATCTATGA
      TTCGTCGACG TCGTCAAGGT CTTCCTCCTG CGGCGTAACT GGTAGATACT
 .....
 901  GATGCTCCAG AACATCTTTG CTATTTTCAG ACAAGATTCA TCTAGCACTG
      CTACGAGGTC TTGTAGAAAC GATAAAAGTC TGTTCTAAGT AGATCGTGAC
 .....
 951  GCTGGAATGA GACTATTGTT GAGAACCTCC TGGCTAATGT CTATCATCAG
      CGACCTTACT CTGATAACAA CTCTTGGAGG ACCGATTACA GATAGTAGTC
 .....
1001  ATAAACCATC TGAAGACAGT CCTGGAAGAA AAACTGGAGA AAGAAGATTT
      TATTTGGTAG ACTTCTGTCA GGACCTTCTT TTTGACCTCT TTCTTCTAAA
 .....
1051  CACCAGGGGA AAACTCATGA GCAGTCTGCA CCTGAAAAGA TATTATGGGA
      GTGGTCCCCT TTTGAGTACT CGTCAGACGT GGACTTTTCT ATAATACCCT
 .....
1101  GGATTCTGCA TTACCTGAAG GCCAAGGAGT ACAGTCACTG TGCCTGGACC
      CCTAAGACGT AATGGACTTC CGGTTCCTCA TGTCAGTGAC ACGGACCTGG
 .....
1151  ATAGTCAGAG TGGAAATCCT AAGGAACTTT TACTTCATTA ACAGACTTAC
      TATCAGTCTC ACCTTTAGGA TTCCTTGAAA ATGAAGTAAT TGTCTGAATG
 .....
1201  AGGTTACCTC CGAAACTGAA GATCTCCTAG CCTGTGCCTC TGGGACTGGA
      TCCAATGGAG GCTTTGACTT CTAGAGGATC GGACACGGAG ACCCTGACCT
 .....
1251  CAATTGCTTC AAGCATTCTT CAACCAGCAG ATGCTGTTTA AGTGACTGAT
      GTTAACGAAG TTCGTAAGAA GTTGGTCGTC TACGACAAAT TCACTGACTA
 .....
1301  GGCTAATGTA CTGCATATGA AAGGACACTA GAAGATTTTG AAATTTTTAT
      CCGATTACAT GACGTATACT TTCCTGTGAT CTTCTAAAAC TTTAAAAATA
 .....
1351  TAAATTATGA GTTATTTTTA TTTATTTAAA TTTTATTTTG GAAAATAAAT
      ATTTAATACT CAATAAAAAT AAATAAATTT AAAATAAAAC CTTTTATTTA
 .....
                                                      XmaI
                                                       ~
                                                      SmaI
                                                       ~
                                                     BamHI
                                                     ------
                                 AvaI                 AvaI
                                ------                 ~
1401  TATTTTTGGT GCAAAAGTCC CTCGAGGCCT AGCGGCCGCC TAGAGGATCC
      ATAAAAACCA CGTTTTCAGG GAGCTCCGGA TCGCCGGCGG ATCTCCTAGG
 .....
      XmaI
      -----
      SmaI
      -----
      AvaI
      -----
1451  CCGGGCGCTA GGCGGCCGCT AGGCCTTTTT GGCCAAGCTC GAATTTCGAG
      GGCCCGCGAT CCGCCGGCGA TCCGGAAAAA CCGGTTCGAG CTTAAAGCTC
 .....
                        XmaI
                       -------
                        SmaI
                       -------
      EcoRI             AvaI     ClaI
      ------           -------  ------
1501  GAATTCGAGC TCGGTACCCG GGGGATCGAT CCGTCCCCCT TTTCCTTTGT
      CTTAAGCTCG AGCCATGGGC CCCCTAGCTA GGCAGGGGGA AAAGGAAACA
 .....
```

FIG. 8. (CONTINUED)

```
1551  CGATATCATG TAATTAGTTA TGTCACGCTT ACATTCACGC CCTCCCCCCA
      GCTATAGTAC ATTAATCAAT ACAGTGCGAA TGTAAGTGCG GGAGGGGGGT
 .....

1601  CATCCGCTCT AACCGAAAAG GAAGGAGTTA GACAACCTGA AGTCTAGGTC
      GTAGGCGAGA TTGGCTTTTC CTTCCTCAAT CTGTTGGACT TCAGATCCAG
 .....

1651  CCTATTTATT TTTTTATAGT TATGTTAGTA TTAAGAACGT TATTTATATT
      GGATAAATAA AAAAATATCA ATACAATCAT AATTCTTGCA ATAAATATAA
 .....

1701  TCAAATTTTT CTTTTTTTTC TGTACAGACG CGTGTACGCA TGTAACATTA
      AGTTTAAAAA GAAAAAAAAG ACATGTCTGC GCACATGCGT ACATTGTAAT
 .....

1751  TACTGAAAAC CTTGCTTGAG AAGGTTTTGG GACGCTCGAA GGCTTTAATT
      ATGACTTTTG GAACGAACTC TTCCAAAACC CTGCGAGCTT CCGAAATTAA
 .....

1801  TGCAAGCTAG CTTGGCGTAA TCATGGTCAT AGCTGTTTCC TGTGTGAAAT
      ACGTTCGATC GAACCGCATT AGTACCAGTA TCGACAAAGG ACACACTTTA
 .....

1851  TGTTATCCGC TCACAATTCC ACACAACATA CGAGCCGGAA GCATAAAGTG
      ACAATAGGCG AGTGTTAAGG TGTGTTGTAT GCTCGGCCTT CGTATTTCAC
 .....

1901  TAAAGCCTGG GGTGCCTAAT GAGTGAGCTA ACTCACATTA ATTGCGTTGC
      ATTTCGGACC CCACGGATTA CTCACTCGAT TGAGTGTAAT TAACGCAACG
 .....

1951  GCTCACTGCC CGCTTTCCAG TCGGGAAACC TGTCGTGCCA GAGATCTCTG
      CGAGTGACGG GCGAAAGGTC AGCCCTTTGG ACAGCACGGT CTCTAGAGAC
 .....

2001  CATTAATGAA TCGGCCAACG CGCGGGGAGA GGCGGTTTGC GTATTGGGCG
      GTAATTACTT AGCCGGTTGC GCGCCCCTCT CCGCCAAACG CATAACCCGC
 .....

2051  CTCTTCCGCT TCCTCGCTCA CTGACTCGCT GCGCTCGGTC GTTCGGCTGC
      GAGAAGGCGA AGGAGCGAGT GACTGAGCGA CGCGAGCCAG CAAGCCGACG
 .....

                    ClaI
                    -------
2101  GGCGAGCGGT ATCAGATCGA TCTCACTCAA AGGCGGTAAT ACGGTTATCC
      CCGCTCGCCA TAGTCTAGCT AGAGTGAGTT TCCGCCATTA TGCCAATAGG
 .....

2151  ACAGAATCAG GGGATAACGC AGGAAAGAAC ATGTGAGCAA AAGGCCAGCA
      TGTCTTAGTC CCCTATTGCG TCCTTTCTTG TACACTCGTT TTCCGGTCGT
 .....

2201  AAAGGCCAGG AACCGTAAAA AGGCCGCGTT GCTGGCGTTT TTCCATAGGC
      TTTCCGGTCC TTGGCATTTT TCCGGCGCAA CGACCGCAAA AAGGTATCCG
 .....

2251  TCCGCCCCCC TGACGAGCAT CACAAAAATC GACGCTCAAG TCAGAGGTGG
      AGGCGGGGGG ACTGCTCGTA GTGTTTTTAG CTGCGAGTTC AGTCTCCACC
 .....

2301  CGAAACCCGA CAGGACTATA AAGATACCAG GCGTTTCCCC CTGGAAGCTC
      GCTTTGGGCT GTCCTGATAT TTCTATGGTC CGCAAAGGGG GACCTTCGAG
 .....

2351  CCTCGTGCGC TCTCCTGTTC CGACCCTGCC GCTTACCGGA TACCTGTCCG
      GGAGCACGCG AGAGGACAAG GCTGGGACGG CGAATGGCCT ATGGACAGGC
 .....

2401  CCTTTCTCCC TTCGGGAAGC GTGGCGCTTT CTCATAGCTC ACGCTGTAGG
      GGAAAGAGGG AAGCCCTTCG CACCGCGAAA GAGTATCGAG TGCGACATCC
 .....

                                                    ApaLI
                                                    ------
2451  TATCTCAGTT CGGTGTAGGT CGTTCGCTCC AAGCTGGGCT GTGTGCACGA
      ATAGAGTCAA GCCACATCCA GCAAGCGAGG TTCGACCCGA CACACGTGCT
 .....
```

FIG. 8. (CONTINUED)

```
2501  ACCCCCCGTT CAGCCCGACC GCTGCGCCTT ATCCGGTAAC TATCGTCTTG
      TGGGGGGCAA GTCGGGCTGG CGACGCGGAA TAGGCCATTG ATAGCAGAAC
 .....
2551  AGTCCAACCC GGTAAGACAC GACTTATCGC CACTGGCAGC AGCCACTGGT
      TCAGGTTGGG CCATTCTGTG CTGAATAGCG GTGACCGTCG TCGGTGACCA
 .....
2601  AACAGGATTA GCAGAGCGAG GTATGTAGGC GGTGCTACAG AGTTCTTGAA
      TTGTCCTAAT CGTCTCGCTC CATACATCCG CCACGATGTC TCAAGAACTT
 .....
2651  GTGGTGGCCT AACTACGGCT ACACTAGAAG GACAGTATTT GGTATCTGCG
      CACCACCGGA TTGATGCCGA TGTGATCTTC CTGTCATAAA CCATAGACGC
 .....
2701  CTCTGCTGAA GCCAGTTACC TTCGGAAAAA GAGTTGGTAG CTCTTGATCC
      GAGACGACTT CGGTCAATGG AAGCCTTTTT CTCAACCATC GAGAACTAGG
 .....
2751  GGCAAACAAA CCACCGCTGG TAGCGGTGGT TTTTTTGTTT GCAAGCAGCA
      CCGTTTGTTT GGTGGCGACC ATCGCCACCA AAAAAACAAA CGTTCGTCGT
 .....
2801  GATTACGCGC AGAAAAAAAG GATCTCAAGA AGATCCTTTG ATCTTTTCTA
      CTAATGCGCG TCTTTTTTTC CTAGAGTTCT TCTAGGAAAC TAGAAAAGAT
 .....
2851  CGGGGTCTGA CGCTCAGTGG AACGAAAACT CACGTTAAGG GATTTTGGTC
      GCCCCAGACT GCGAGTCACC TTGCTTTTGA GTGCAATTCC CTAAAACCAG
 .....
2901  ATGAGATTAT CAAAAAGGAT CTTCACCTAG ATCCTTTTAA ATTAAAAATG
      TACTCTAATA GTTTTTCCTA GAAGTGGATC TAGGAAAATT TAATTTTTAC
 .....
2951  AAGTTTTAAA TCAATCTAAA GTATATATGA GTAAACTTGG TCTGACAGTT
      TTCAAAATTT AGTTAGATTT CATATATACT CATTTGAACC AGACTGTCAA
 .....
3001  ACCAATGCTT AATCAGTGAG GCACCTATCT CAGCGATCTG TCTATTTCGT
      TGGTTACGAA TTAGTCACTC CGTGGATAGA GTCGCTAGAC AGATAAAGCA
 .....
3051  TCATCCATAG TTGCCTGACT CCCCGTCGTG TAGATAACTA CGATACGGGA
      AGTAGGTATC AACGGACTGA GGGGCAGCAC ATCTATTGAT GCTATGCCCT
 .....
3101  GGGCTTACCA TCTGGCCCCA GTGCTGCAAT GATACCGCGA GACCCACGCT
      CCCGAATGGT AGACCGGGGT CACGACGTTA CTATGGCGCT CTGGGTGCGA
 .....
3151  CACCGGCTCC AGATTTATCA GCAATAAACC AGCCAGCCGG AAGGGCCGAG
      GTGGCCGAGG TCTAAATAGT CGTTATTTGG TCGGTCGGCC TTCCCGGCTC
 .....
3201  CGCAGAAGTG GTCCTGCAAC TTTATCCGCC TCCATCCAGT CTATTAATTG
      GCGTCTTCAC CAGGACGTTG AAATAGGCGG AGGTAGGTCA GATAATTAAC
 .....
3251  TTGCCGGGAA GCTAGAGTAA GTAGTTCGCC AGTTAATAGT TTGCGCAACG
      AACGGCCCTT CGATCTCATT CATCAAGCGG TCAATTATCA AACGCGTTGC
 .....
3301  TTGTTGCCAT TGCTACAGGC ATCGTGGTGT CACGCTCGTC GTTTGGTATG
      AACAACGGTA ACGATGTCCG TAGCACCACA GTGCGAGCAG CAAACCATAC
 .....
3351  GCTTCATTCA GCTCCGGTTC CCAACGATCA AGGCGAGTTA CATGATCCCC
      CGAAGTAAGT CGAGGCCAAG GGTTGCTAGT TCCGCTCAAT GTACTAGGGG
 .....
3401  CATGTTGTGC AAAAAAGCGG TTAGCTCCTT CGGTCCTCCG ATCGTTGTCA
      GTACAACACG TTTTTTCGCC AATCGAGGAA GCCAGGAGGC TAGCAACAGT
 .....
3451  GAAGTAAGTT GGCCGCAGTG TTATCACTCA TGGTTATGGC AGCACTGCAT
      CTTCATTCAA CCGGCGTCAC AATAGTGAGT ACCAATACCG TCGTGACGTA
 .....
```

FIG. 8. (CONTINUED)

```
3501  AATTCTCTTA CTGTCATGCC ATCCGTAAGA TGCTTTTCTG TGACTGGTGA
      TTAAGAGAAT GACAGTACGG TAGGCATTCT ACGAAAAGAC ACTGACCACT
.....
3551  GTACTCAACC AAGTCATTCT GAGAATAGTG TATGCGGCGA CCGAGTTGCT
      CATGAGTTGG TTCAGTAAGA CTCTTATCAC ATACGCCGCT GGCTCAACGA
.....
3601  CTTGCCCGGC GTCAATACGG GATAATACCG CGCCACATAG CAGAACTTTA
      GAACGGGCCG CAGTTATGCC CTATTATGGC GCGGTGTATC GTCTTGAAAT
.....
3651  AAAGTGCTCA TCATTGGAAA ACGTTCTTCG GGGCGAAAAC TCTCAAGGAT
      TTTCACGAGT AGTAACCTTT TGCAAGAAGC CCCGCTTTTG AGAGTTCCTA
.....
                                              ApaLI
                                              -------
3701  CTTACCGCTG TTGAGATCCA GTTCGATGTA ACCCACTCGT GCACCCAACT
      GAATGGCGAC AACTCTAGGT CAAGCTACAT TGGGTGAGCA CGTGGGTTGA
.....
3751  GATCTTCAGC ATCTTTTACT TTCACCAGCG TTTCTGGGTG AGCAAAAACA
      CTAGAAGTCG TAGAAAATGA AAGTGGTCGC AAAGACCCAC TCGTTTTTGT
.....
3801  GGAAGGCAAA ATGCCGCAAA AAAGGGAATA AGGGCGACAC GGAAATGTTG
      CCTTCCGTTT TACGGCGTTT TTTCCCTTAT TCCCGCTGTG CCTTTACAAC
.....
3851  AATACTCATA CTCTTCCTTT TTCAATATTA TTGAAGCATT TATCAGGGTT
      TTATGAGTAT GAGAAGGAAA AAGTTATAAT AACTTCGTAA ATAGTCCCAA
.....
3901  ATTGTCTCAT GAGCGGATAC ATATTTGAAT GTATTTAGAA AAATAAACAA
      TAACAGAGTA CTCGCCTATG TATAAACTTA CATAAATCTT TTTATTTGTT
.....
3951  ATAGGGGTTC CGCGCACATT TCCCCGAAAA GTGCCACCTG ACGTCTAAGA
      TATCCCCAAG GCGCGTGTAA AGGGGCTTTT CACGGTGGAC TGCAGATTCT
.....
4001  AACCATTATT ATCATGACAT TAACCTATAA AAATAGGCGT ATCACGAGGC
      TTGGTAATAA TAGTACTGTA ATTGGATATT TTTATCCGCA TAGTGCTCCG
.....
4051  CCTTTCGTCT CGCGCGTTTC GGTGATGACG GTGAAAACCT CTGACACATG
      GGAAAGCAGA GCGCGCAAAG CCACTACTGC CACTTTTGGA GACTGTGTAC
.....
4101  CAGCTCCCGG AGACGGTCAC AGCTTGTCTG TAAGCGGATG CCGGGAGCAG
      GTCGAGGGCC TCTGCCAGTG TCGAACAGAC ATTCGCCTAC GGCCCTCGTC
.....
4151  ACAAGCCCGT CAGGGCGCGT CAGCGGGTGT TGGCGGGTGT CGGGGCTGGC
      TGTTCGGGCA GTCCCGCGCA GTCGCCCACA ACCGCCCACA GCCCCGACCG
.....
                                            ApaLI
                                            -------
4201  TTAACTATGC GGCATCAGAG CAGATTGTAC TGAGAGTGCA CCATATCGAC
      AATTGATACG CCGTAGTCTC GTCTAACATG ACTCTCACGT GGTATAGCTG
.....
4251  GCTCTCCCTT ATGCGACTCC TGCATTAGGA AGCAGCCCAG TAGTAGGTTG
      CGAGAGGGAA TACGCTGAGG ACGTAATCCT TCGTCGGGTC ATCATCCAAC
.....
4301  AGGCCGTTGA GCACCGCCGC CGCAAGGAAT GGTGCATGCA AGGAGATGGC
      TCCGGCAACT CGTGGCGGCG GCGTTCCTTA CCACGTACGT TCCTCTACCG
.....
4351  GCCCAACAGT CCCCCGGCCA CGGGGCCTGC CACCATACCC ACGCCGAAAC
      CGGGTTGTCA GGGGGCCGGT GCCCCGGACG GTGGTATGGG TGCGGCTTTG
.....
4401  AAGCACTAAT AGGAATTGAT TTGGATGGTA TAAACGGAAA CAAAAAAAAG
      TTCGTGATTA TCCTTAACTA AACCTACCAT ATTTGCCTTT GTTTTTTTTC
.....
```

FIG. 8. (CONTINUED)

```
4451  AGCTGGTACT ACTTTCTTTA AAATTATTTT ATTATTTGAT TTTATTTAAT
      TCGACCATGA TGAAAGAAAT TTTAATAAAA TAATAAACTA AAATAAATTA
.....
4501  AGTATATATT ATATTTTGAA CGTAGATTAT TTTGTTGAAA GTTGCTGTAG
      TCATATATAA TATAAAACTT GCATCTAATA AAACAACTTT CAACGACATC
.....
4551  TGCCATTGAT TCGTAACACT AATTCTGTAT TAGTCATTCC TCTTGTTTGA
      ACGGTAACTA AGCATTGTGA TTAAGACATA ATCAGTAAGG AGAACAAACT
.....
4601  TAGTATCCAA AAAAACGGCT ATTTTTTTGC AATCTTATTT CCTGCATATT
      ATCATAGGTT TTTTTGCCGA TAAAAAAACG TTAGAATAAA GGACGTATAA
.....
4651  ATACAGATAA CATAATGAAA GAAAAAATCT TTTTTTTTGT TCTTCAATGA
      TATGTCTATT GTATTACTTT CTTTTTTAGA AAAAAAAACA AGAAGTTACT
.....
4701  TGATTTCAAC CATTCTTTTA AACATTGATC AATTCCTGAG CAACAACCCC
      ACTAAAGTTG GTAAGAAAAT TTGTAACTAG TTAAGGACTC GTTGTTGGGG
.....
4751  ATACACACTG GTTTATATAC CGCCCCTTTT ACAGTTGAAG AAAGAAATAG
      TATGTGTGAC CAAATATATG GCGGGGAAAA TGTCAACTTC TTTCTTTATC
.....
4801  AAATAGAAAT AGCAAACAAA AGATATGACA GTCAACACTA AGACCTATAG
      TTTATCTTTA TCGTTTGTTT TCTATACTGT CAGTTGTGAT TCTGGATATC
.....
4851  TGAGAGAGCA GAAACTCATG CCTCACCAGT AGCACAGCGA TTATTTCGAT
      ACTCTCTCGT CTTTGAGTAC GGAGTGGTCA TCGTGTCGCT AATAAAGCTA
.....
4901  TAATGGAACT GAAGAAAACC AATTTATGTG CATCAATTGA CGTTGATACC
      ATTACCTTGA CTTCTTTTGG TTAAATACAC GTAGTTAACT GCAACTATGG
.....
                  AvaI
                  ------
4951  ACTAAGGAGT TCCTCGAGTT AATTGATAAA TTAGGTCCTT ATGTATGCTT
      TGATTCCTCA AGGAGCTCAA TTAACTATTT AATCCAGGAA TACATACGAA
.....
5001  AATCAAGACT CATATTGATA TAATCAATGA TTTTTCCTAT GAATCCACTA
      TTAGTTCTGA GTATAACTAT ATTAGTTACT AAAAAGGATA CTTAGGTGAT
.....
5051  TTGAACCATT ATTAGAACTT TCACGTAAAC ATCAATTTAT GATTTTTGAA
      AACTTGGTAA TAATCTTGAA AGTGCATTTG TAGTTAAATA CTAAAAACTT
.....
5101  GATAGAAAAT TTGCTGATAT TGGTAATACC GTAAAGAAAC AATATATTGG
      CTATCTTTTA AACGACTATA ACCATTATGG CATTTCTTTG TTATATAACC
.....
5151  TGGAGTTTAT AAAATTAGTA GTTGGGCAGA TATTACCAAT GCTCATGGTG
      ACCTCAAATA TTTTAATCAT CAACCCGTCT ATAATGGTTA CGAGTACCAC
.....
5201  TCACTGGGAA TGGAGTGGTT GAAGGATTAA AACAGGGAGC TAAAGAAACC
      AGTGACCCTT ACCTCACCAA CTTCCTAATT TTGTCCCTCG ATTTCTTTGG
.....
5251  ACCACCAACC AAGAGCCAAG AGGGTTATTG ATGTTAGCTG AATTATCATC
      TGGTGGTTGG TTCTCGGTTC TCCCAATAAC TACAATCGAC TTAATAGTAG
.....
5301  AGTGGGATCA TTAGCATATG GAGAATATTC TCAAAAAACT GTTGAAATTG
      TCACCCTAGT AATCGTATAC CTCTTATAAG AGTTTTTTGA CAACTTTAAC
.....
5351  CTAAATCCGA TAAGGAATTT GTTATTGGAT TTATTGCCCA ACGTGATATG
      GATTTAGGCT ATTCCTTAAA CAATAACCTA AATAACGGGT TGCACTATAC
.....
```

FIG. 8. (CONTINUED)

```
5401  GGTGGCCAAG AAGAAGGATT TGATTGGCTT ATTATGACAC CTGGAGTTGG
      CCACCGGTTC TTCTTCCTAA ACTAACCGAA TAATACTGTG GACCTCAACC

5451  ATTAGATGAT AAAGGTGATG GATTAGGACA ACAATATAGA ACTGTTGATG
      TAATCTACTA TTTCCACTAC CTAATCCTGT TGTTATATCT TGACAACTAC

5501  AAGTTGTTAG CACTGGAACT GATATTATCA TTGTTGGTAG AGGATTGTTT
      TTCAACAATC GTGACCTTGA CTATAATAGT AACAACCATC TCCTAACAAA

5551  GGTAAAGGAA GAGATCCAGA TATTGAAGGT AAAAGGTATA GAAATGCTGG
      CCATTTCCTT CTCTAGGTCT ATAACTTCCA TTTTCCATAT CTTTACGACC

5601  TTGGAATGCT TATTTGAAAA AGACTGGCCA ATTATAAATG TGAAGGGGGA
      AACCTTACGA ATAAACTTTT TCTGACCGGT TAATATTTAC ACTTCCCCCT

5651  GATTTTCACT TTATTAGATT TGTATATATG TAGAATAAAT AAATAAATAA
      CTAAAAGTGA AATAATCTAA ACATATATAC ATCTTATTTA TTTATTTATT

5701  GTTAAATAAA TAATTAAATA AGGGTGGTAA TTATTACTAT TTACAATCAA
      CAATTTATTT ATTAATTTAT TCCCACCATT AATAATGATA AATGTTAGTT

5751  AGGTGGTCCT TCTAGCTGTA ATCCGGGCAG CGCAACGGAA CATTCATCAG
      TCCACCAGGA AGATCGACAT TAGGCCCGTC GCGTTGCCTT GTAAGTAGTC

5801  TGTAAAAATG GAATCAATAA AGCCCTGCGC TCATGAGCCC GAAGTGGCGA
      ACATTTTTAC CTTAGTTATT TCGGGACGCG AGTACTCGGG CTTCACCGCT

5851  GCCCGATCTT CCCCATCGGT GATGTCGGCG ATATAGGCGC CAGCAACCGC
      CGGGCTAGAA GGGGTAGCCA CTACAGCCGC TATATCCGCG GTCGTTGGCG

5901  ACCTGTGGCG CCGCAGCGCG CAGGGTCAGC CTGAATACGC GTTTAATGAC
      TGGACACCGC GGCGTCGCGC GTCCCAGTCG GACTTATGCG CAAATTACTG

5951  CAGCACAGTC GTGATGGCAA GGTCAGAATA GCCCAAGTCG GCCGAGGGGC
      GTCGTGTCAG CACTACCGTT CCAGTCTTAT CGGGTTCAGC CGGCTCCCCG

6001  CTGTACAGTG AGGGAAGATC TGATATTGAC GAAGAGGAAC CAATGTAACG
      GACATGTCAC TCCCTTCTAG ACTATAACTG CTTCTCCTTG GTTACATTGC

6051  TTACACTGAA GAAAACACAC AATAAACGGG AAGAAACGGT GTAAAAGTGT
      AATGTGACTT CTTTTGTGTG TTATTTGCCC TTCTTTGCCA CATTTTCACA

6101  GAAAATAATT TTTGAATATC ATTTCCCTTG GTTTAATTCC AAACGAAACG
      CTTTTATTAA AAACTTATAG TAAAGGGAAC CAAATTAAGG TTTGCTTTGC

                          EcoRI
                          ------
6151  TGTTTTTTTT AGAGAATGGG AATTCTTATT GGATGTCTAG ATTGTTTGTT
      ACAAAAAAAA TCTCTTACCC TTAAGAATAA CCTACAGATC TAACAAACAA

                ApaLI
                ------
6201  TACTCCAGAC TGTGCACAAA AACGTTTGGA TGGATGATCA GAAGATATTT
      ATGAGGTCTG ACACGTGTTT TTGCAAACCT ACCTACTAGT CTTCTATAAA

6251  TTAGGCTTAG CTCTAAATAT AAGAAATGAT GCTTGAAAAA CCAGACAGAA
      AATCCGAATC GAGATTTATA TTCTTTACTA CGAACTTTTT GGTCTGTCTT

6301  ATTGAGTTTC AAAAATTGGT AATGTGAGGT ATTAGTCAAC TAACCAAATA
      TAACTCAAAG TTTTTAACCA TTACACTCCA TAATCAGTTG ATTGGTTTAT
```

FIG. 8. (CONTINUED)

```
6351  ACAATGCAAA CCGGTTGATA CATTTCATTT TGAAAATAAT GAAACTGGAA
      TGTTACGTTT GGCCAACTAT GTAAAGTAAA ACTTTTATTA CTTTGACCTT
.....
6401  TTGGATGACC AGCACACAAA CACATAAAGT AATTATGGGA ATTAGAAGCG
      AACCTACTGG TCGTGTGTTT GTGTATTTCA TTAATACCCT TAATCTTCGC
.....
6451  AACATAGAGG AGTACTTGGC CACGAACAGA ATACAAGTGG GAACACTATT
      TTGTATCTCC TCATGAACCG GTGCTTGTCT TATGTTCACC CTTGTGATAA
.....
6501  TTCTCCATTG TTTTAGTTCT GTTTTTTTGT CAGCCTAGTT TTGTGCTATG
      AAGAGGTAAC AAAATCAAGA CAAAAAAACA GTCGGATCAA AACACGATAC
.....
                              HindIII
                              ------
6551  TGTAAAAAAT ATTGCCAAGA AAAAAAGCTT GTTTTGTGGC CAGTGTCCGA
      ACATTTTTTA TAACGGTTCT TTTTTTCGAA CAAAACACCG GTCACAGGCT
.....
6601  AAAAAATTTT GGGGAATCTT CGGATTAATT TATGTTTTCA
      TTTTTTAAAA CCCCTTAGAA GCCTAATTAA ATACAAAAGT
.....
```

FIG. 9.

ATGTATGTTTATAAGAGAGATGGCCGTAAAGAGCCAGTACGTTTCGACAAAAT
CACTGCCAGAGTTCAAAGATTATGTTA
CGGTTTGAATCCAAACCACGTTGAACCAGTTGCTATTACCCAAAAAGTTATATC
AGGTGTTTACCAGGGGGTTACTACTA
TTGAGTTGGACAACTTGGCTGCAGAAATTGCTGCTACAATGACAACAATTCAC
CCAGATTACGCTGTCTTAGCCGCTAGA
ATTGCCGTATCAAATTTACATAAGCAAACCACCAAACAGTATTCCAAAGTGTC
TAAGGATTTATATGAATACATTAATCC
TAAGACTGGGTTACACTCTCCTATGATTTCCAAGGAAACCTACGACATCATTAT
GGAACACGAAGATGAATTAAACTCAG
CCATTGTTTACGACAGAGATTTTAACTACAATTATTTTGGGTTCAAGACTTTGG
AAAGATCATATTTGTTACGTATCAAC
GGTAAGGTTGCTGAAAGACCACAACATTTGATCATGAGGGTTGCTGTCGGTAT
TCACGGTAATGATATACCAAGGGTCAT
TGAAACCTATAACTTGATGTCTCAAAGATTCTTCACCCATGGTTCTCCTTGTTTA
TTTAACGCTGGTACACCAAGACCAC
AAATGTCCTCATGTTTCTTGCTTGCTATGAAGGATGATTCTATTGAAGGTATTT
ACGACACTTTGAAATCGTGTGCTTTG
ATCTCAAAAAGTGCTGGAGGAATCGGTTTACACATCCACAACATTCGTTCTACC
GGTGCTTACATTGCTGGTACCAATGG
TACTTCTAATGGTATTATTCCAATGGTAAGAGTATTCAATAACACTGCACGTTA
TGTCGACCAAGGTGGTAACAAGAGAC
CTGGTGCCTTTGCCTTGTACTTAGAACCATGGCACAGTGACATTTTTGATTTCA
TTGATATTAGAAAGAATCACGGTAAA
GAAGAAATCAGAGCCAGAGATTTGTTCCCAGCTTTGTGGATTCCAGATTTGTTC
ATGAAAAGAGTTGAACAAAATGGTGA
CTGGACTTTATTCTCACCAAATGAGGCCCCAGGCTTGGCTGATGTTTATGGTGA
CGAATTCGAAGAATTATACACCAAAT
ACGAAAAAGAAAACCGTGGTAGACAGACCATCAAAGCTCAAAAATTGTGGTA
TGCTATTTTGGGAGCCCAAACTGAAACA
GGTACCCCATTTATGTTATATAAAGATTCATGTAACAACAAATCCAACCAAAA
GAACTTGGGTATTATCAAATCTTCCAA
CTTGTGTTGTGAAATTGTTGAATATTCTGCTCCAGATGAAGTTGCTGTTTGTAA
CTTGGCTTCCATTGCCTTGCCATCAT
TTGTTGAAAATGATGAAAAAAGTACTTGGTACAACTTTGACAAATTACATCAG
GTCACTAAGGTTGTCACCCGTAACTTG
AACAGAGTTATTGACCGTAACCATTACCCAGTCCCAGAAGCTGAAAGATCAAA
CATGAGACACAGACCAATTGCTTTGGG
TGTTCAAGGTTTGGCTGATGCCTTTATGGAATTGAGATTACCATTTGACTCTCA
AGAAGCTAGAGAATTGAACATTCAAA

FIG. 9. (CONTINUED)

TTTTTGAGACTATCTACCATGCTGCTGTTGAAGCTTCAATTGAATTGGCTAAAG
AAGAAGGTGCCTACGAAACCTATCCA
GGTTCTCCAGCCTCTCAAGGTTTATTACAATTTGATTTGTGGAACAGAAAACCA
ACTGAATTATGGGATTGGGATACATT
AAAACAAGATTTGGCCAAACATGGTATGAGAAACTCCTTGTTGGTTGCACCAA
TGCCTACTGCTTCCACATCACAAATTT
TGGGTAACAATGAATGTTTTGAACCATACACTTCTAACATTTACTCTAGAAGAG
TATTAGCTGGAGAATTCCAAATTGTC
AATCCATATTTATTGAAGGACTTGGTTGATTTGGGTGTCTGGAACGACGCTATG
AAAAGTAGTATTATTGCTAACAATGG
TTCTATCCAAGCCTTACCAAACATCCCTGATGAAATCAAGGCATTGTACAAAA
CTGTCTGGGAAATCTCACAAAAACATA
TTATCGACATGGCTGCTGATAGAGCAGCATTTATTGATCAATCTCAATCATTAA
ACATTCACATCAAAGATCCAACAATG
GGTAAATTAACCAGTATGCACTTCTACGGTTGGAAGAAAGGTTTAAAGACTGG
TATGTACTACTTAAGAACACAAGCTGC
CAGTGCTGCTATTCAATTTACCATTGATCAAAAGATTGCTGAGACTGCCGGTCA
TACGGTTGCAAACTTGGACAAATTAA

ACATTAAGAAATATGTTAACAAAGGAAGAGTTGAGAGTGAGAATACCAGTGAT
GCTCCATACAAGTCACCATCAACCGAA
CCAACCTCATTAGAAAGTTCAGTTGCTGATTTGAAAATAAAAGATGAAGGTGA
AAAGCCAGCTGAAGACAAAACCATTGA
AGAACTCGAAAATGACATTTATAGTGCCAAAGTTATCGCATGTGCTATTGATA
ATCCAGAATCTTGTACAATGTGTTCTG
GT

FIG. 10.

FIG. 11.

FIG. 12.

CCCCGTTAACCACTTCTAGGGTATACCATTTCATCTGACTGAATAACTGGTTAG
TCGATTTGTTGTTGAAGAAAAGTGAC
CACCTAGTTTTTTCTGCCAACATTTTTTGCGATGAGCCGTCGACGCGTTGTCTTT
TTCTACCCCACGTTTAACAATCTTG
CCAGTCAATTCCCTAGCCAAATAAACTTTAGACTCACAACTCTAACACTGACTC
GTGCCCCCCTGTTTAAACTCTAAATT
ACTTCACAGAGCCTTTACTACCTTAAATTTARGRTTWTSKAKKGTTTCTGTTTTT
TTGCAAATCACCCTGACTYGTTTTT
TTTTCAGCCAGGTTTTTCGTTAAAATCTGACCAAAAAATTTACRACTCCTATWT
TTAAAACTCYAAAWWACAATTAAAAC
TCAATTCAGACAAGTCCTTCTGCTCATTCTGAGTCTTCTCTATTGTCTTTTGACT
TTTTGTGTGTGACTATTTTCATGAT
CACCCCGTTTCTTGCATTTTTTTTCAGTCAACTTTTTCTCAAAATCAAGCCAAAAA
AACACACCTTTAACTACCTATACAA
CGCAAACCTATTCAAAACA

FIG. 13.

ATGACTACTTCCAAGGAAACTTTCCTTTTCACTTCAGAATCCGTTGGTGAAGGT
CACCCAGATAAGATTTGTGACCAAGT
CTCCGATGCCATTTTAGATGCTTGTTTAGCTGTTGATCCATTGTCAAAAGTTGCT
TGTGAAACTGCTGCCAAAACCGGTA
TGATTATGGTTTTTGGTGAAATTACCACTAAAGCTCAATTGGATTATCAAAAAA
TCATTAGAGACACCATTAAACACATT
GGTTACGACGATTCTGAAAAAGGTTTTGATTACAAGACTTGTAACGTCTTGGTT
GCAATTGAACAACAATCTCCAGATAT
TGCTCAAGGTTTACATTACGAAAAAGCTTTGGAAGAGTTGGGTGCTGGTGATC
AAGGTATTATGTTTGGTTATGCCACCG
ATGAAACCGATGAAAAATTGCCATTGACCATTTTATTGGCCCACAAATTGAAT
GCTGCCTTGGCTTCTGCCAGAAGATCA
GGTTCCTTGCCATGGTTGAGACCAGATACCAAAACCCAAGTCACCATCGAGTA
TGAAAAAGATGGTGGTGCAGTTATCCC
AAAAAGAGTCGACACAATTGTTATTTCCACTCAACATGCCGAAGAAATCACCA
CCGAAAATTTGAGAAAAGAAATTATTG
AACATATCATCAAGCAAGTCATCCCAGAACATTTATTAGACGACAAAACTATC
TACCACATTCAGCCATCAGGCAGATTC
GTCATTGGTGGTCCCCAAGGTGATGCTGGTTTGACTGGTAGAAAGATCATTGTT
GACACCTATGGTGGTTGGGGTGCACA
TGGTGGTGGTGCCTTCTCAGGCAAGGATTTCTCCAAAGTTGATAGGTCTGCTGC
TTATGCCGCTCGGTGGGTTGCTAAGT
CGTTGGTGACCGCCGGATTGGCCAAAAGGGCCTTGGTGCAGTTCTCCTATGCTA
TTGGGGTTGCTGAACCCACCAGCATT
TATATAGACACCTATGGGACATCTAAATTGAGCACCGAAGCCCTTGTAGAAAT
TATCAAGAATAATTTTGACTTACGCCC
TGGCGTAATTGTAAAAGAATTAGATTTGGCTCGTCCTATTTATTTTAAAACCGC
TTCTTACGGACATTTTACTAACCAAG
AAAATTCTTGGGAACAACCAAAAAAATTAAAATTT

FIG. 14.

```
  1 MYVYKRDGRK EPVRFDKITA RVQRLCYGLN PRHVEPVAIT QKVISGVYQG
 51 VCTIELDNLA AEIAATMCTI HPDYAVLAAR IAVSNLHKQT TKQYSKVSKD
101 LYEYINPKTG LHSPMISKET YDIIMEHEDE LNSAIVYDRD FNYNYFGFKT
151 LERSYLLRIN GKVAERPQHL IMRVAVGIHG NDIPRVIETY NLMSQRFFTH
201 GSPCLFNAGT PRPQMSSCFL LAMKDDSIEG IYDTLKSCAL ISKSAGGIGL
251 HIHNIRSTGA YIAGTNGTSN GIIPMVRVFN NTARYVDQGG NKRPGAFALY
301 LEPWHSDIFD FIDIRKNHGK EEIRARDLFP ALWIPDLFMK RVEQNGLWTL
351 FSPNEAPGLA DVYGDEFEEL YTRYEKENRG RQTIKAQKLW YAILGAQTET
401 GTFFMLYKDS CNRKSNQKNL GIIKSSNLCC EIVEYSAPDE VAVCNLASIA
451 LPSFVENDEK STNVNFDKLK QVTKVVTRNL NRVIDRNHYP VPEAERSNMR
501 HRPIALGVQG LQAFMELRL PFDSQEAREL NIQIFETIYH AAVEASIELA
551 KEEGAYETYP GSPASQGLLQ FDLNNRKPTE LWDWDTLKQD LAKHGMRNSL
601 LVAPMPTAST SQILGNNECF EPYTSNIYSR RVLAGEFQIV NPYLLKDLVD
651 LGVWNDAMKS SIINNGSIQ ALPNIPDEIK ALYKTVWEIS QKHIIDMAAD
701 RAAFIDQSQS LNIHIKDPTN GKLTSMHFYG WKKGLKTGMY YLRTQAASAA
751 IQFTIDQKIA ETAGHTVAIL DKLNIKKYVN KGRVEEENTS DAPYKSFSTE
801 PTSLESSVAC LKIKDEGEKP AEDKTIEELE NDIYSAKVIA CAIDNPESCT
851 MCSG
```

FIG. 15.

```
  1 MTTSKETFLF TEESVGEGHP DKICDQVSDA ILDACLAVDP LSKVACETAA
 51 KTGMIMVFGE ITTKAQLDYQ KIVRDTIKHI GYDDSEKGFD YKTCNVLVAI
101 EQQSPDIAQG LNYEKALEEL GAGDQGIMFG YATDETDEKL PLTILLAHKL
151 NAALASARES GSLPWLRPDT KTQVTIEYEK DGGAVIPKRV DTIVISTQHA
201 EEITTENLRK EIIEKIIKQV IPEHLLDDKT IYHIQPSGRF VIGGPQGDAG
251 LTGRKIIVDT YGGWGAHGGG AFSGKDFSKV DRSAAYAARW VAKSLVTAGL
301 AKRALVQFSY AIGVAEPTSI YIDTYGTSKL STEALVEIIK NNFDLRPGVI
351 VKELDLARPI YFKTASYGHF TNQEMSWEQP KKLKF
```

FIG. 16.

RH170498 AF101-AF150 (16 hours
glucose/maltose vs galactose/maltose
AF110

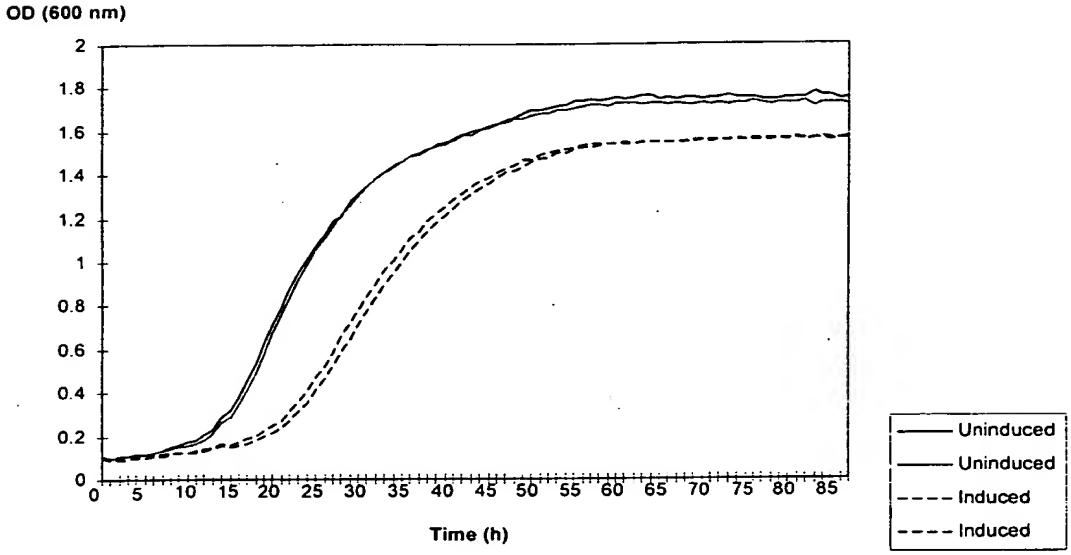


FIG. 17.

C. albicans library screening experiment 28/11/97
glucose/maltose vs galactose/maltose
genom. sample 113g

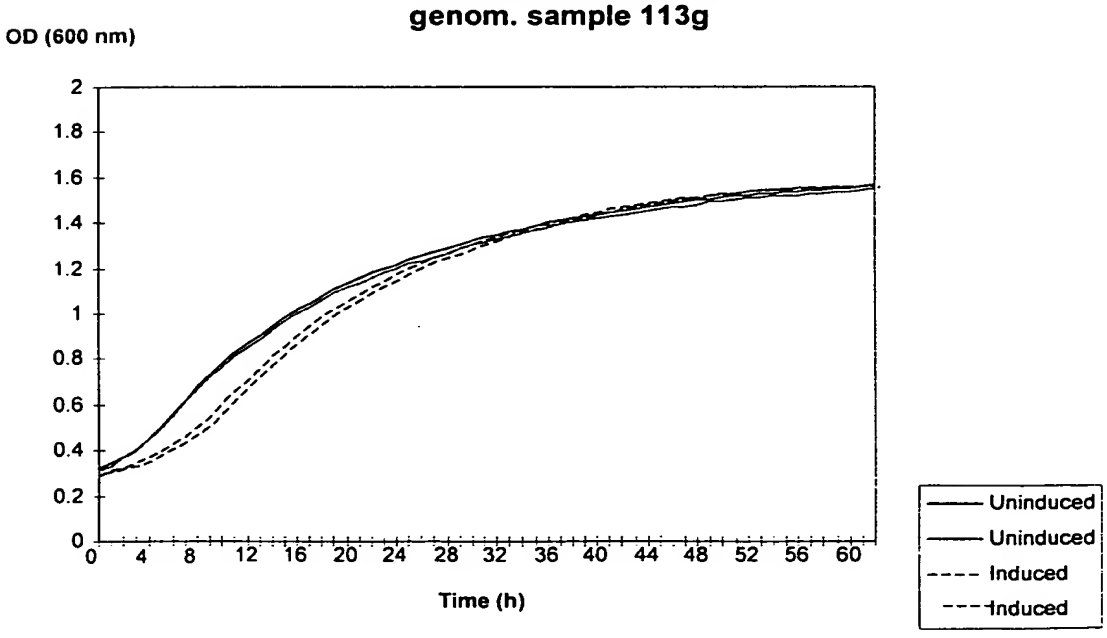


FIG. 18.

RH170498 AF101-AF150 (16 hours induction).
glucose/maltose vs galactose/maltose
AF117

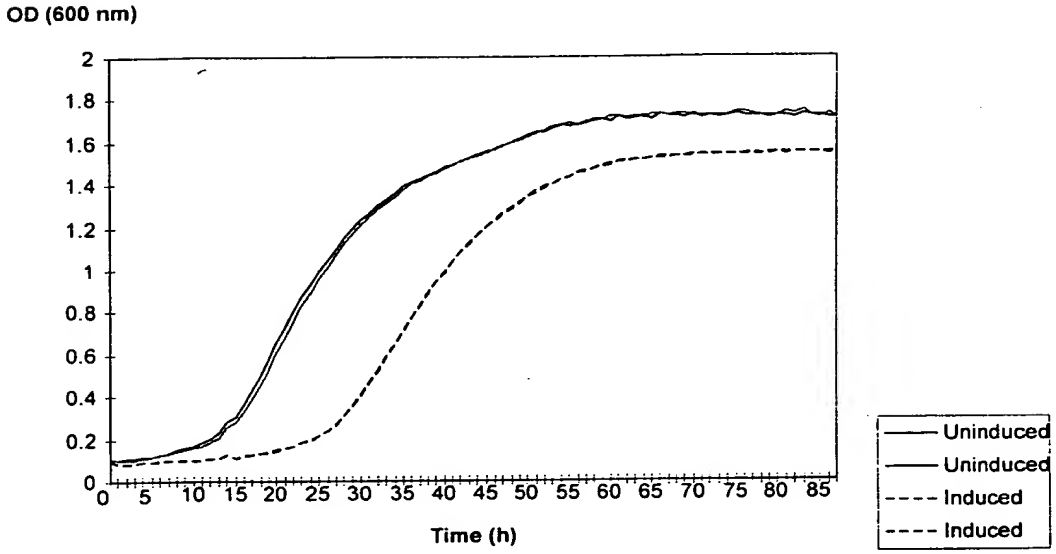


FIG. 19.

C. albicans library screening experiment 28/11/97
glucose/maltose vs galactose/maltose
genom. sample 135g

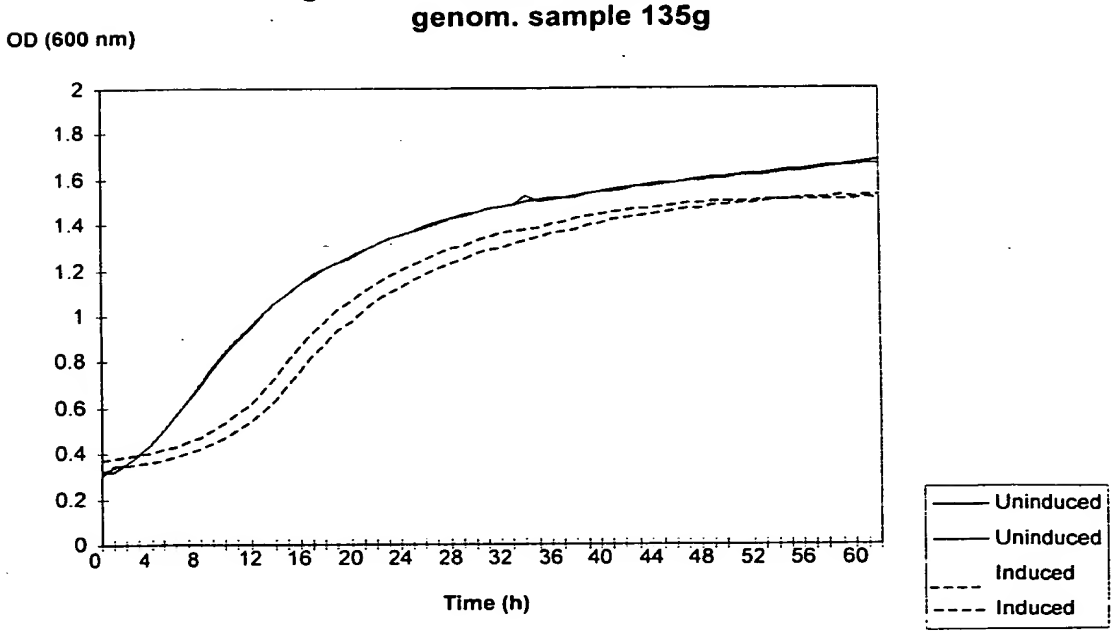


FIG. 20.

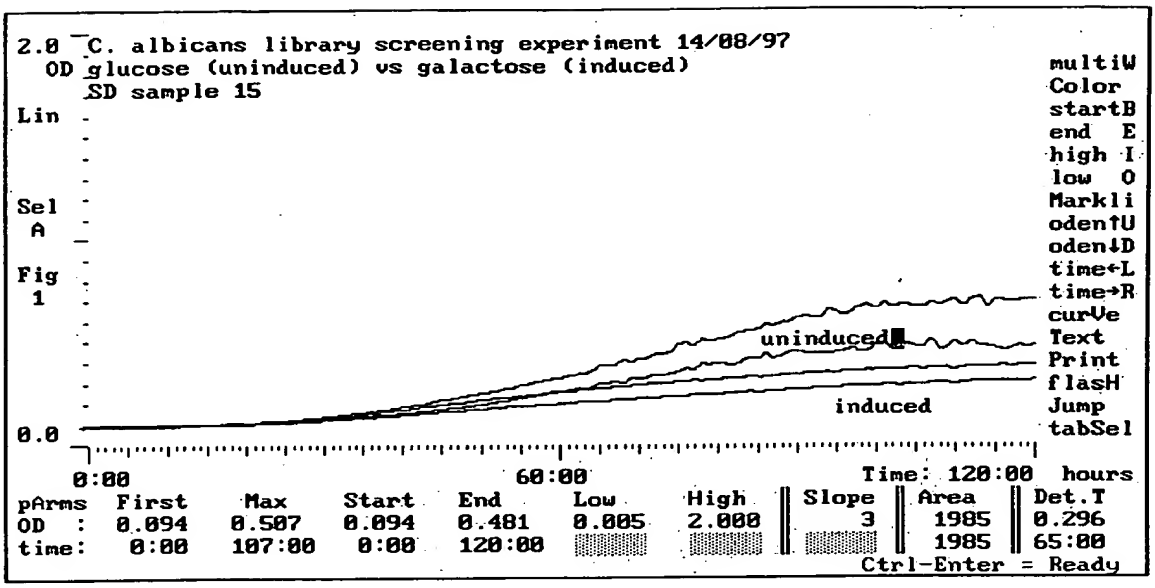
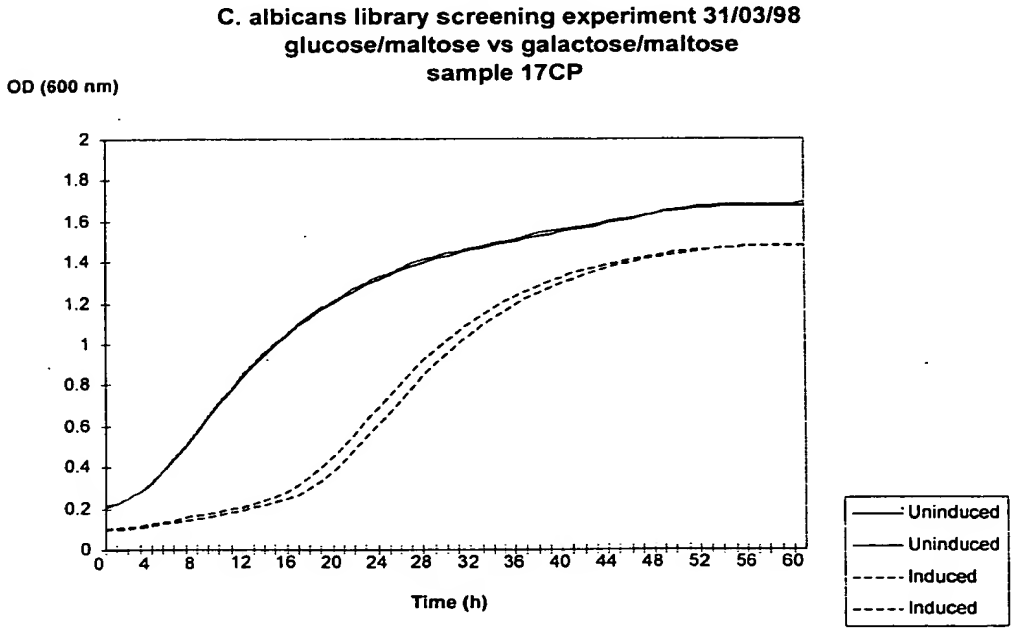

2.0
C. albicans library screening experiment 14/08/97
OD glucose (uninduced) vs galactose (induced)
SD sample 15
Lin
Sel
A
Fig
1
uninduced
induced
0.0
0:00
60:00
Time: 120:00 hours
multiW
Color
startB
end E
high I
low O
Markli
odenUU
odenDD
timeLL
timeRR
curVe
Text
Print
flasH
Jump
tabSel
pArms First Max Start End Low High Slope Area Det.T
OD : 0.094 0.507 0.094 0.481 0.005 2.000 3 1985 0.296
time: 0:00 107:00 0:00 120:00 1985 65:00
Ctrl-Enter = Ready

FIG. 21.


C. albicans library screening experiment 31/03/98
glucose/maltose vs galactose/maltose
sample 17CP
OD (600 nm)
2
1.8
1.6
1.4
1.2
1
0.8
0.6
0.4
0.2
0
0 4 8 12 16 20 24 28 32 36 40 44 48 52 56 60
Time (h)
Uninduced
Uninduced
Induced
Induced

38/75

FIG. 22.

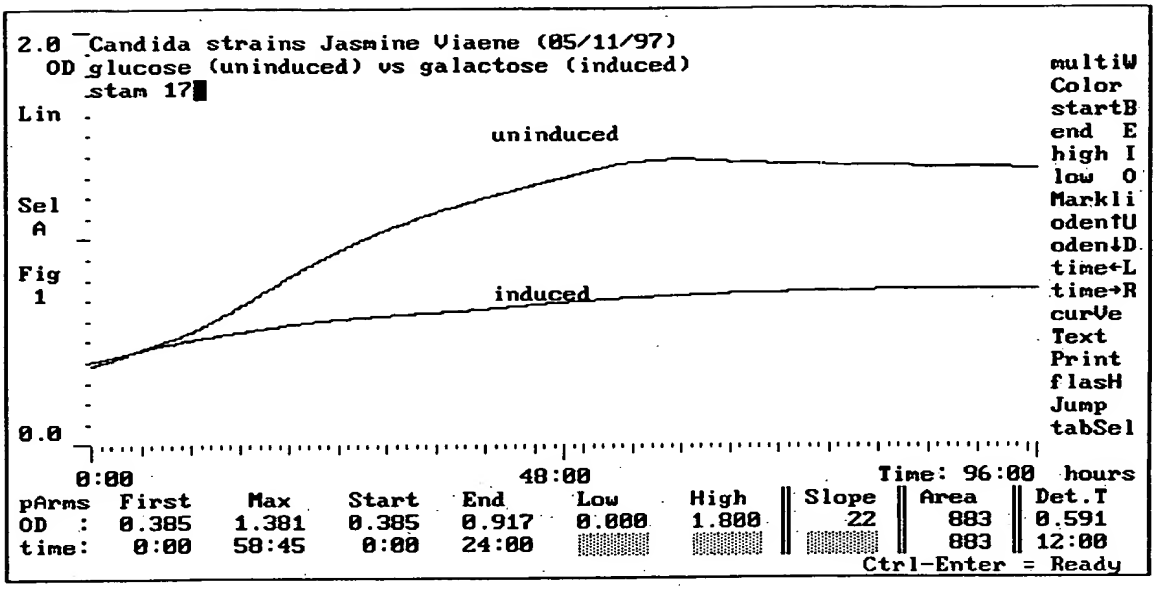


FIG. 23.

C. albicans library screening experiment 15/12/97
glucose vs galactose
genom. sample 190g

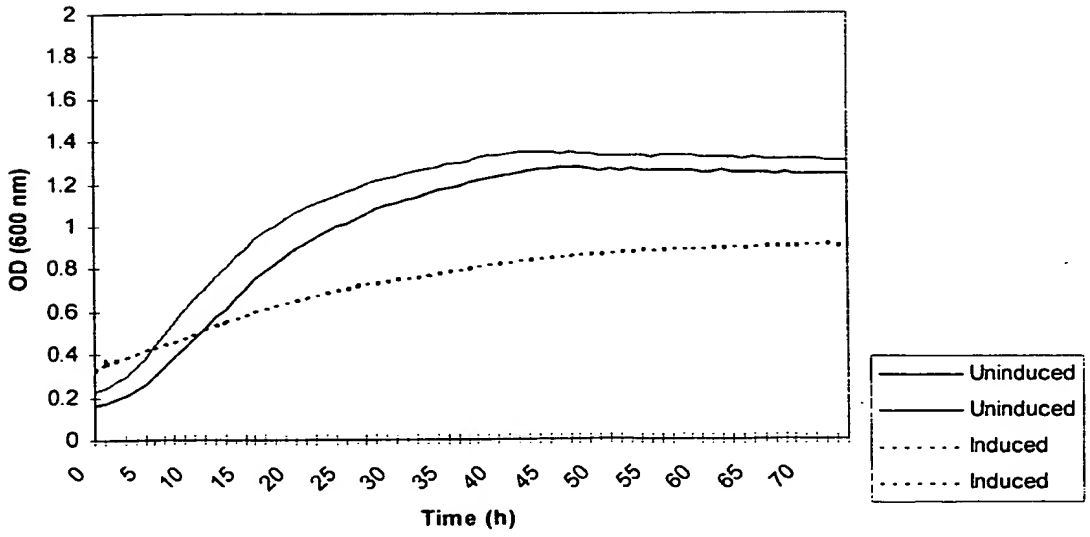


FIG. 24.

C. albicans library screening experiment 15/12/97
glucose vs galactose
genom. sample 207g

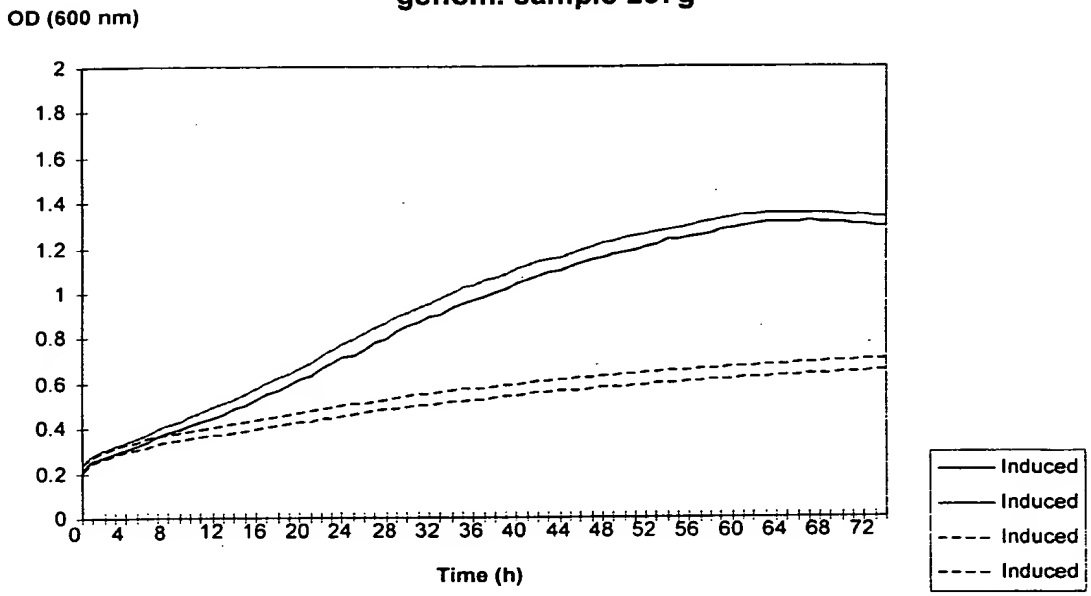


FIG. 25.

CP211-234+AF231-254 28/04/98 IVR
glucose/maltose vs galactose/maltose
sample CP214

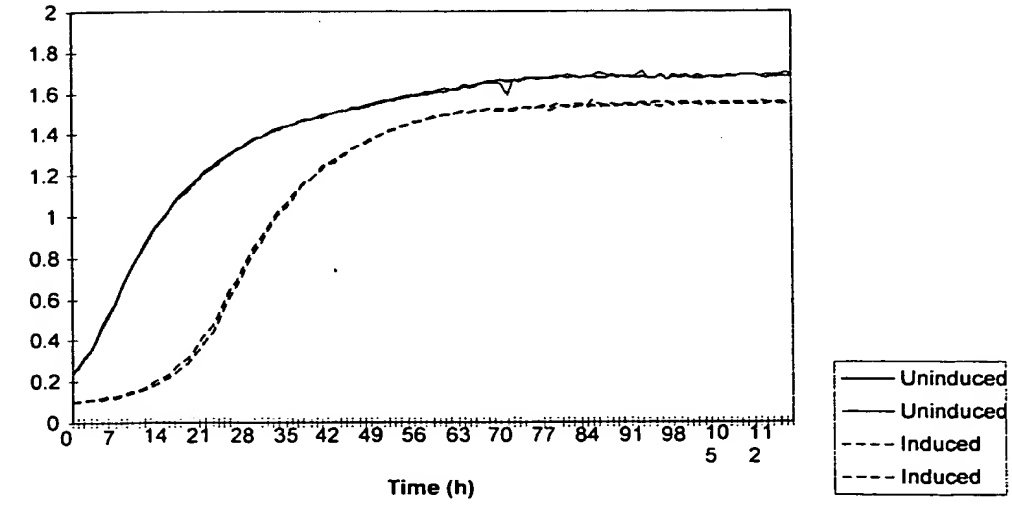


FIG. 26.

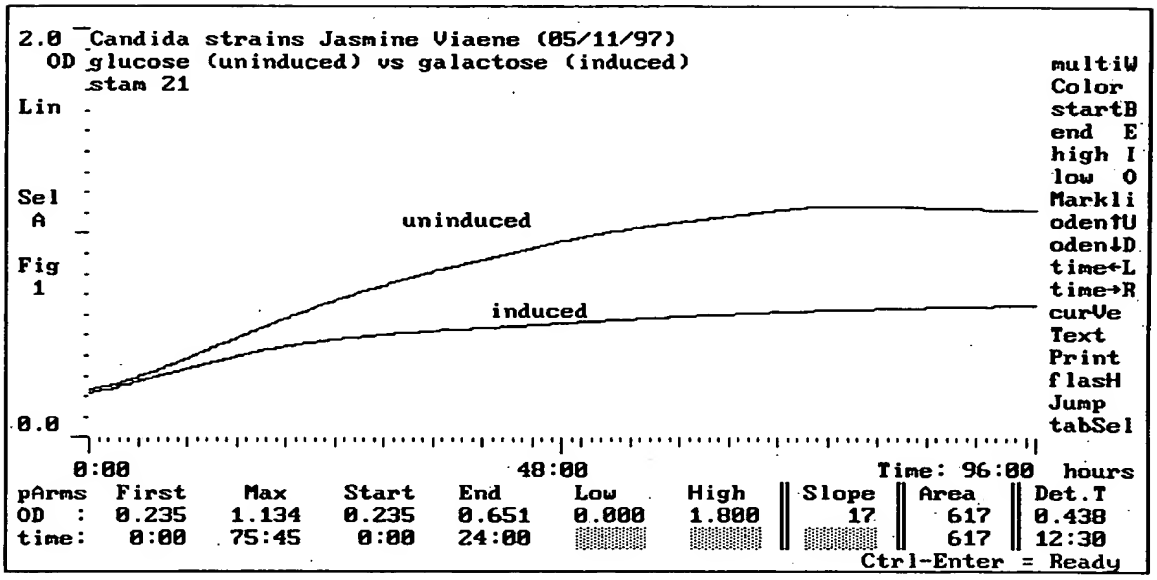

2.0
OD
Lin
Sel
A
Fig
1
0.0
Candida strains Jasmine Viaene (05/11/97)
glucose (uninduced) vs galactose (induced)
stam 21
uninduced
induced
multiW
Color
startB
end E
high I
low O
Markli
odenfU
oden↓D
time←L
time→R
curVe
Text
Print
flasH
Jump
tabSel
0:00
48:00
Time: 96:00 hours
pArms First Max Start End Low High Slope Area Det.T
OD : 0.235 1.134 0.235 0.651 0.000 1.800 17 617 0.438
time: 0:00 75:45 0:00 24:00 617 12:30
Ctrl-Enter = Ready

FIG. 27.

C. albicans library screening experiment 15/12/97
glucose vs galactose
genom. sample 222g

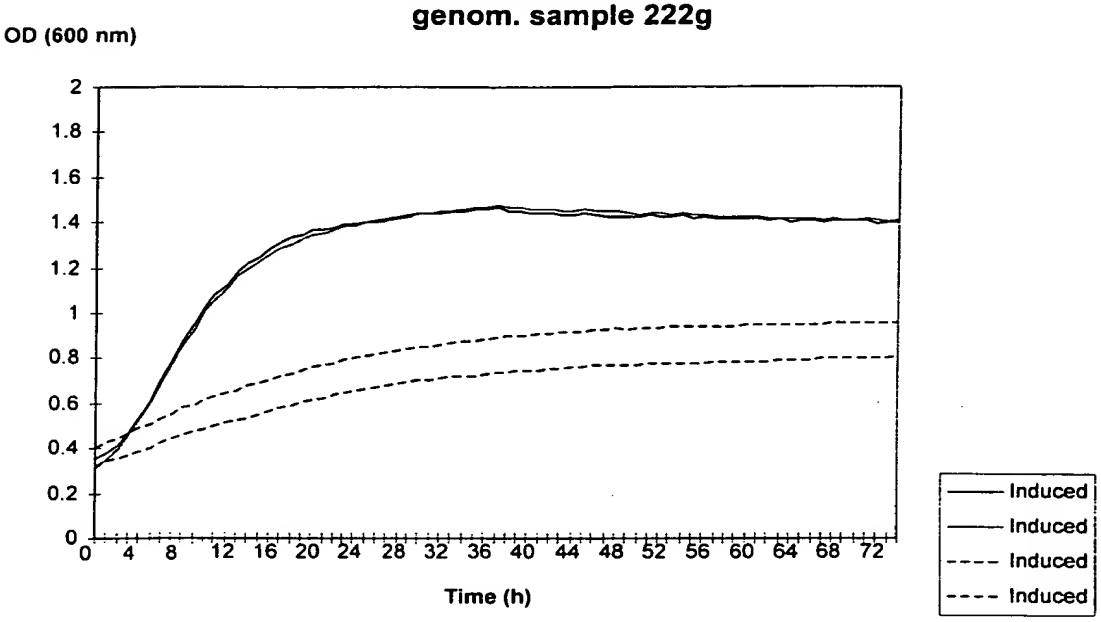


FIG. 28.

C. albicans library screening experiment 19/12/97
glucose/maltose vs galactose/maltose
genom. sample 222g

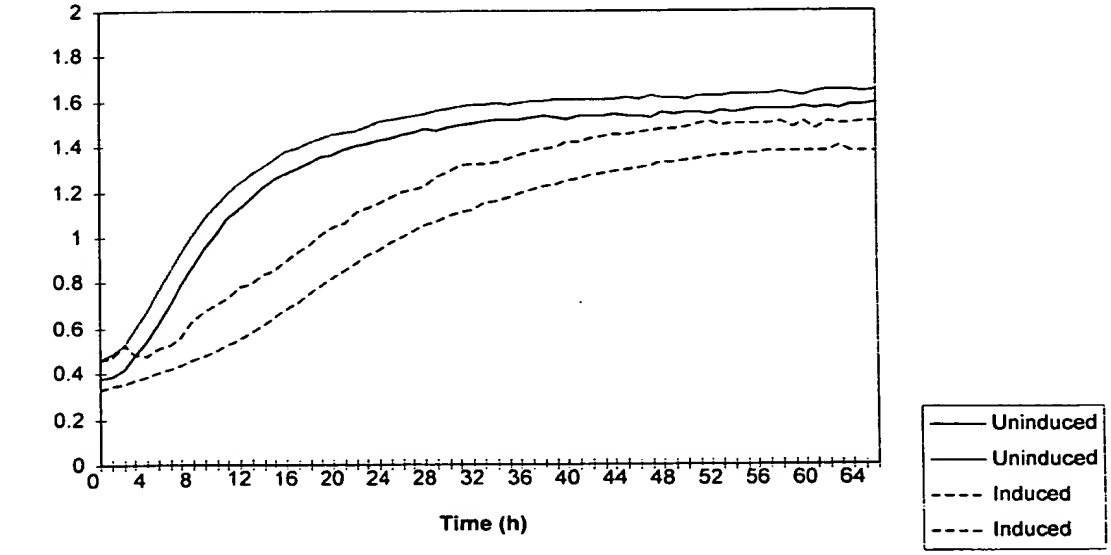


FIG. 29.

CP211-234+AF231-254 28/04/98
glucose/maltose vs galactose/maltose
sample CP223

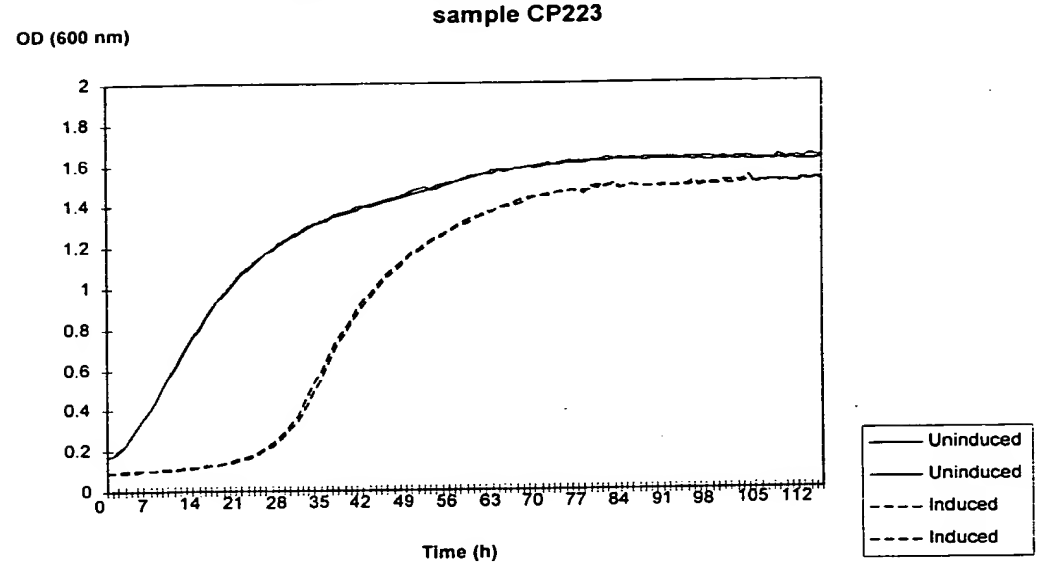


FIG. 30.

C. albicans library screening experiment 24/04/98
glucose/maltose vs galactose/maltose
sample 226af

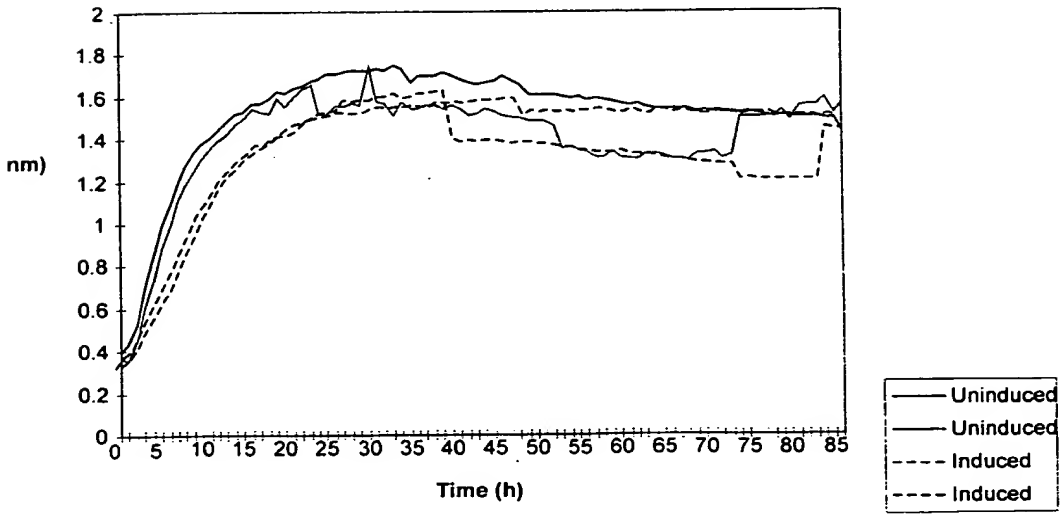


FIG. 31.

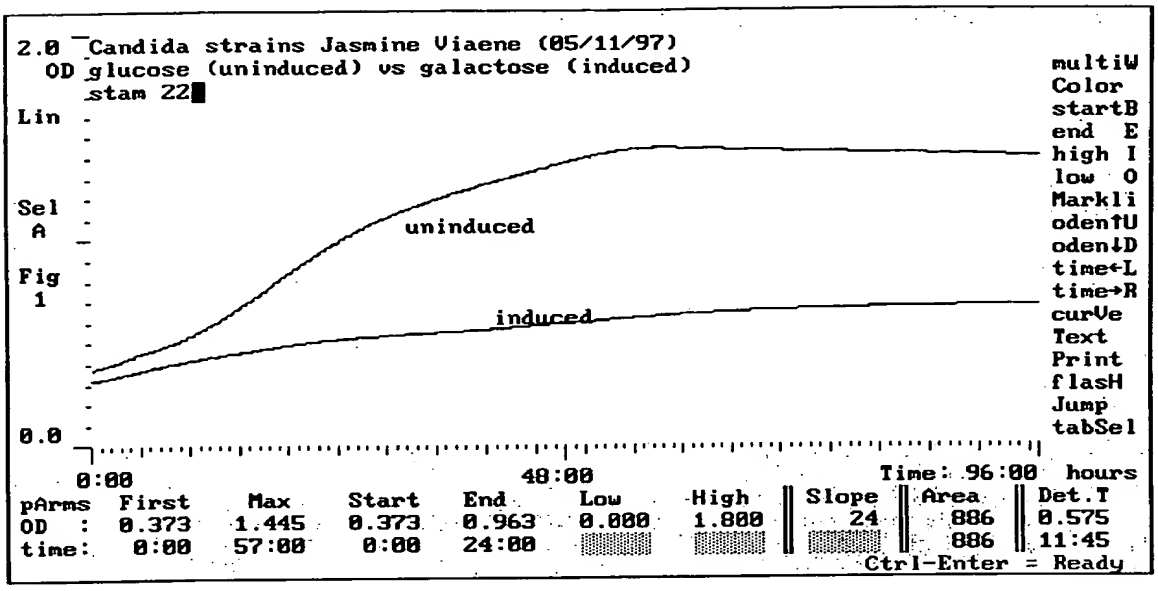

2.0
OD
Lin
Sel
A
Fig
1
0.0
Candida strains Jasmine Viaene (05/11/97)
glucose (uninduced) vs galactose (induced)
stam 22
uninduced
induced
multiW
Color
startB
end E
high I
low O
Markli
odenUU
odenDD
timeL
timeR
curVe
Text
Print
flasH
Jump
tabSel
0:00
48:00
Time: 96:00 hours
pArms First Max Start End Low High Slope Area Det.T
OD : 0.373 1.445 0.373 0.963 0.000 1.800 24 886 0.575
time: 0:00 57:00 0:00 24:00 886 11:45
Ctrl-Enter = Ready

FIG. 32.

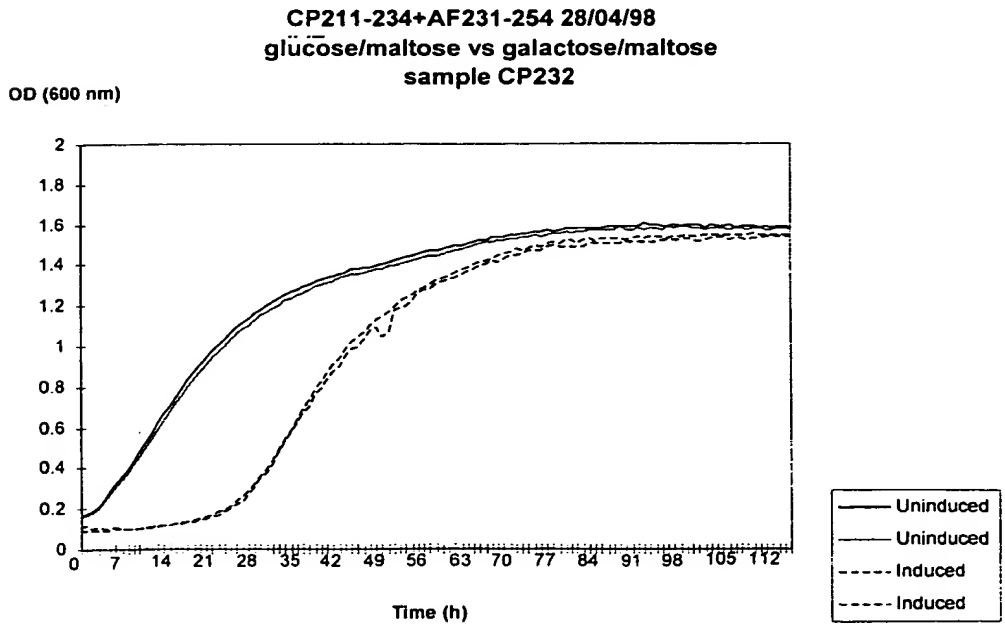

CP211-234+AF231-254 28/04/98
glucose/maltose vs galactose/maltose
sample CP232
OD (600 nm)
2
1.8
1.6
1.4
1.2
1
0.8
0.6
0.4
0.2
0
0 7 14 21 28 35 42 49 56 63 70 77 84 91 98 105 112
Time (h)
Uninduced
Uninduced
Induced
Induced

FIG. 33.

CP211-234+AF231-254 28/04/98
glucose/maltose vs galactose/maltose
sample CP233

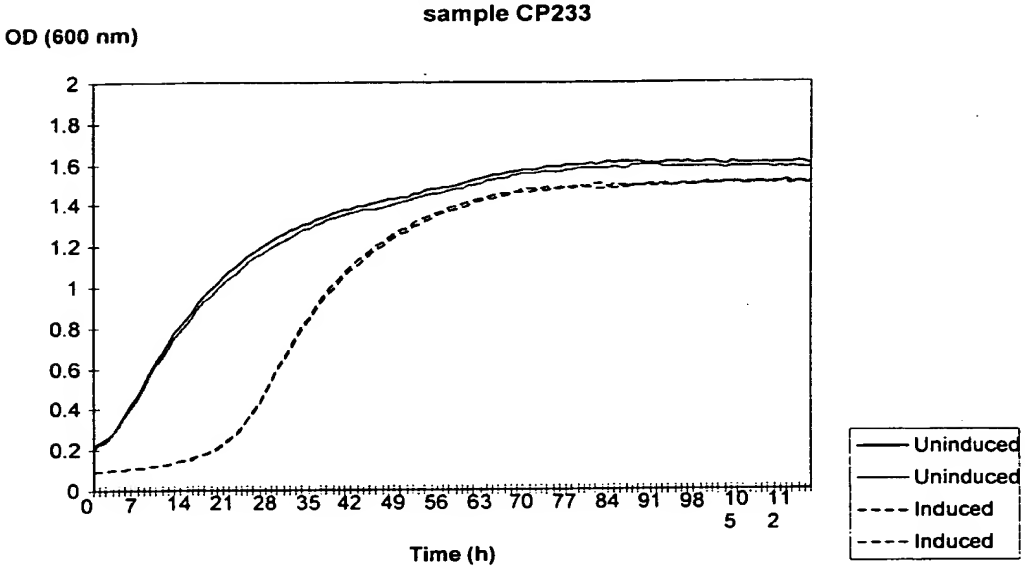


FIG. 34.

CP211-234+AF231-254 28/04/98 IVR
glucose/maltose vs galactose/maltose
sample AF249

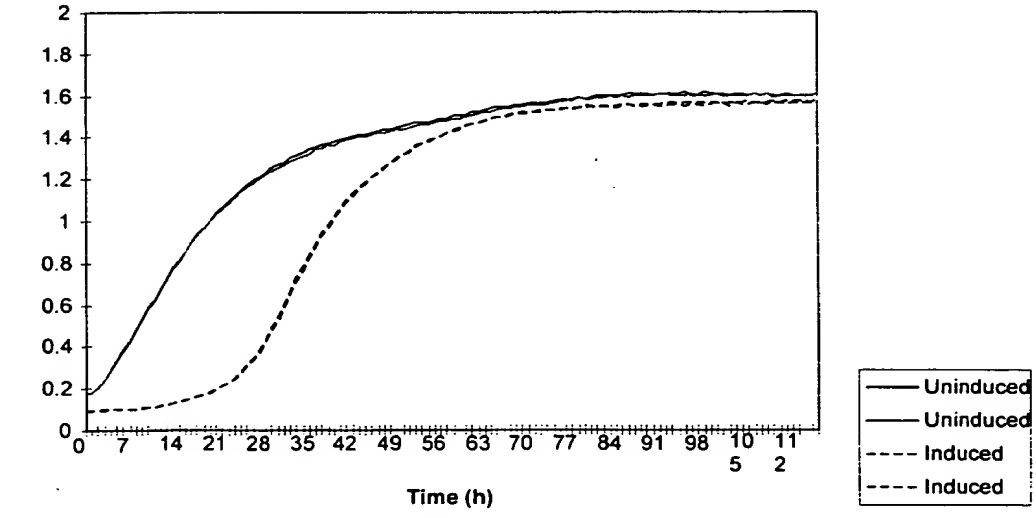


FIG. 35.

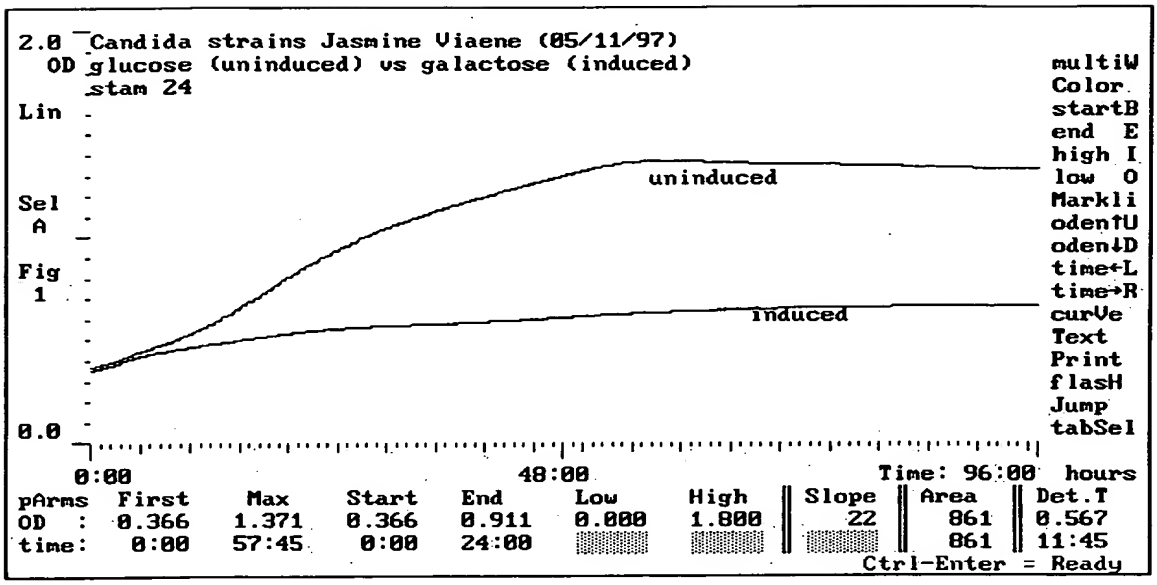

2.0 Candida strains Jasmine Viaene (05/11/97)
OD glucose (uninduced) vs galactose (induced)
stam 24
Lin
Sel A
Fig 1
0.0
uninduced
induced
multiW
Color
startB
end E
high I
low O
Markli
odenUU
odenDD
timeLL
timeRR
curVe
Text
Print
flasH
Jump
tabSel
0:00
48:00
Time: 96:00 hours
pArms First Max Start End Low High Slope Area Det.T
OD : 0.366 1.371 0.366 0.911 0.000 1.800 22 861 0.567
time: 0:00 57:45 0:00 24:00 861 11:45
Ctrl-Enter = Ready

FIG. 36.

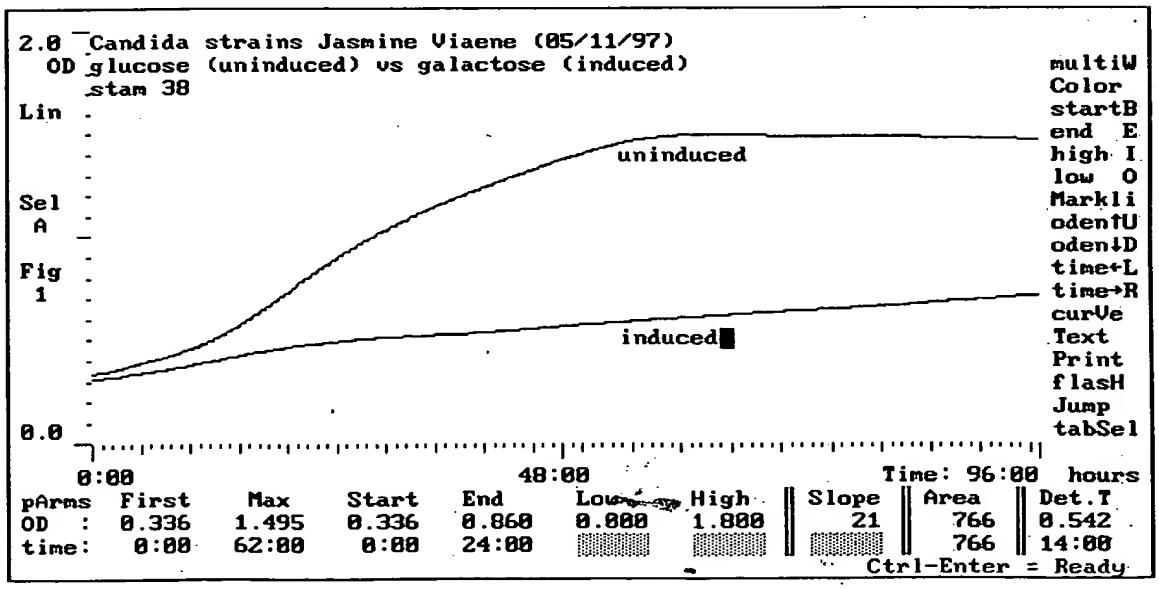

2.0 Candida strains Jasmine Viaene (05/11/97)
OD glucose (uninduced) vs galactose (induced)
stam 38
Lin
Sel A
Fig 1
0.0
uninduced
induced
multiW
Color
startB
end E
high I
low O
Markli
odenUU
odenDD
timeLL
timeRR
curVe
Text
Print
flasH
Jump
tabSel
0:00
48:00
Time: 96:00 hours
pArms First Max Start End Low High Slope Area Det.T
OD : 0.336 1.495 0.336 0.860 0.000 1.800 21 766 0.542
time: 0:00 62:00 0:00 24:00 766 14:00
Ctrl-Enter = Ready

FIG. 37.

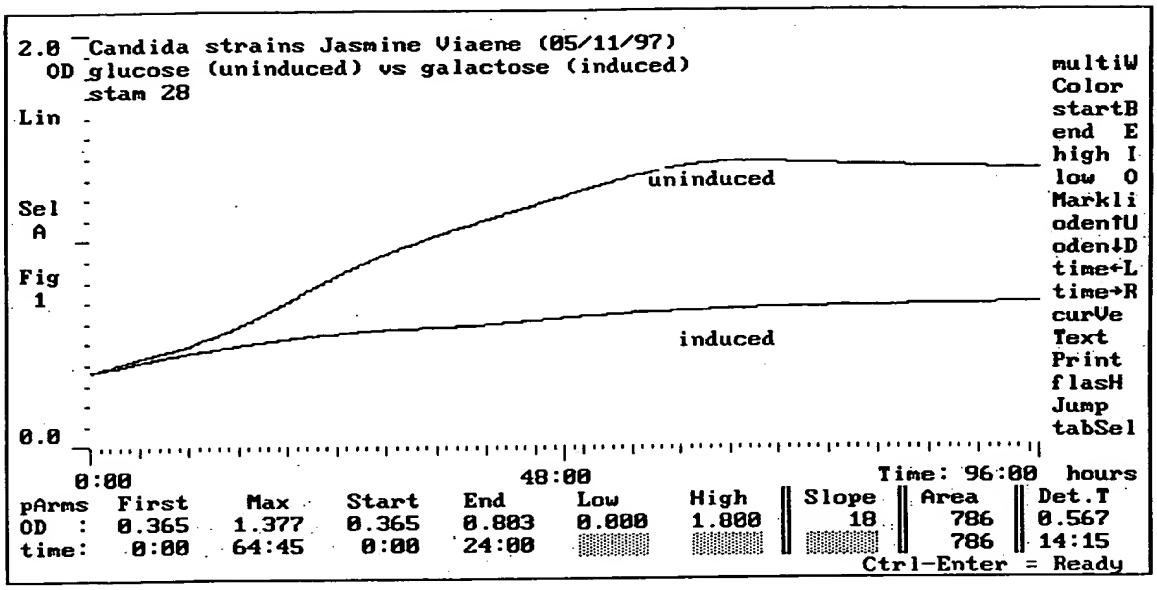


FIG. 38.

C. albicans library screening experiment 27/10/97
glucose vs galactose
YPD sample 328

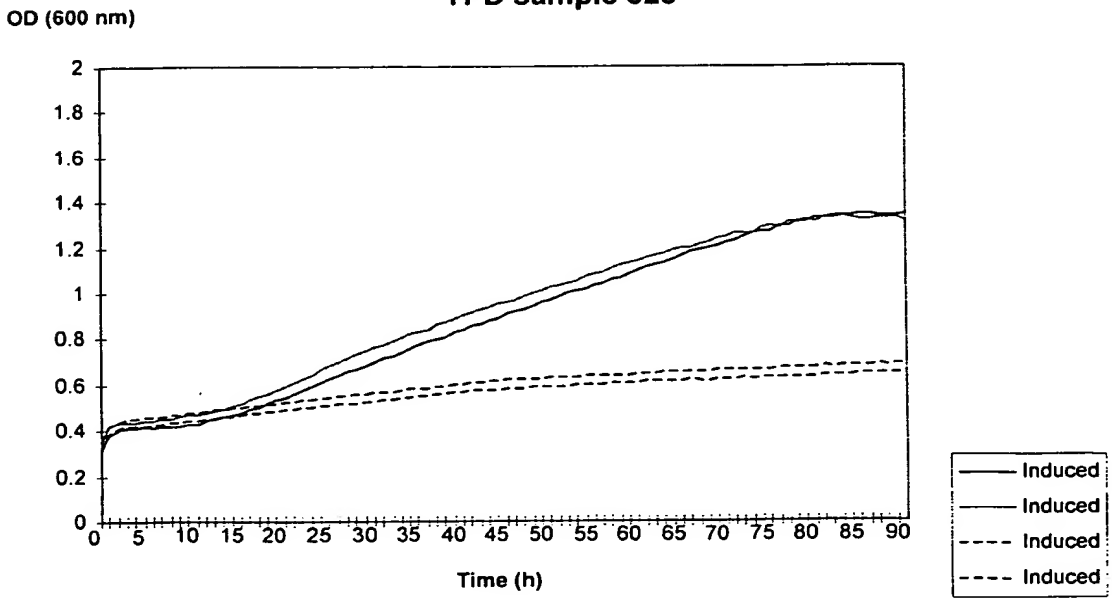


FIG. 39

C. albicans cDNA library screening 12-02-98
glucose/maltose vs galactose/maltose
YPD sample 357

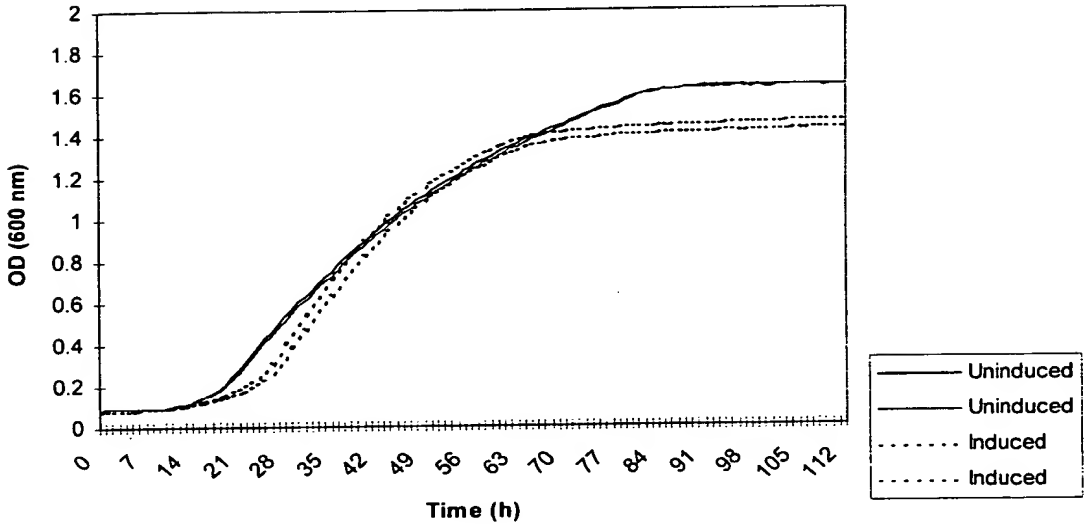


FIG. 40

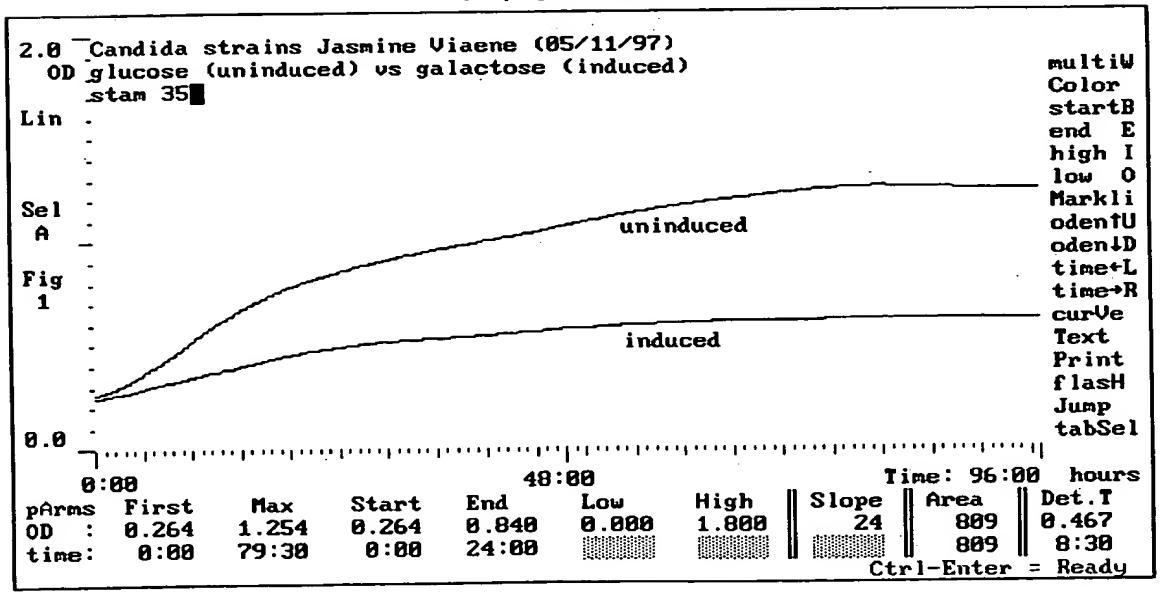


FIG. 41.

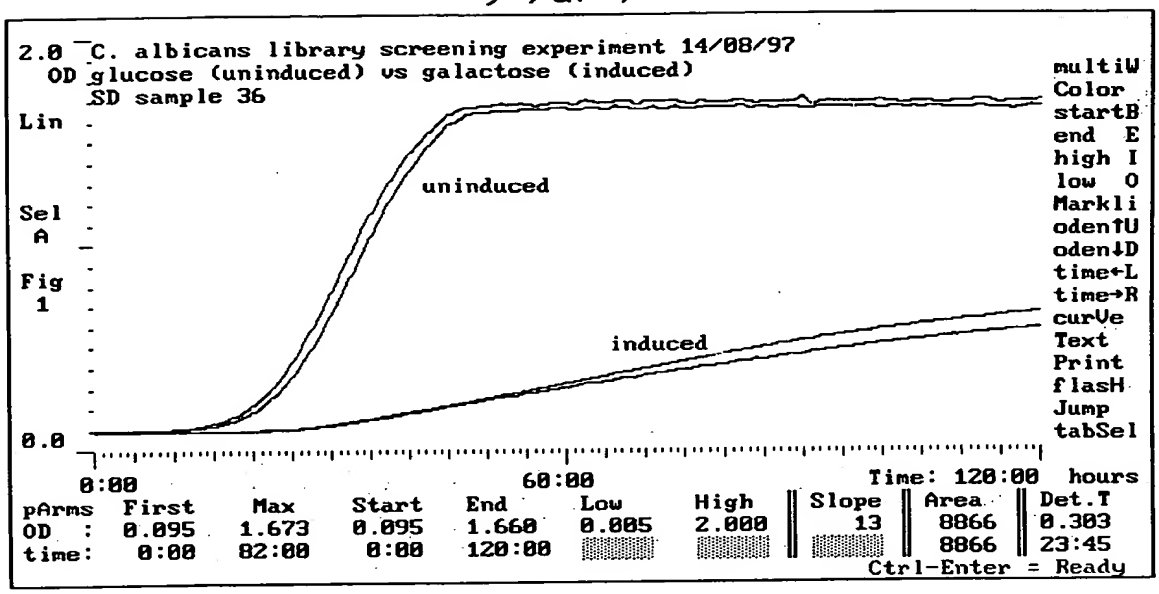

2.0 C. albicans library screening experiment 14/08/97
OD glucose (uninduced) vs galactose (induced)
SD sample 36
Lin
Sel A
Fig 1
uninduced
induced
0.0
0:00
60:00
Time: 120:00 hours
multiW
Color
startB
end E
high I
low O
Markli
odenUU
odenDD
timeLL
timeRR
curVe
Text
Print
flasH
Jump
tabSel
pArms First Max Start End Low High Slope Area Det.T
OD : 0.095 1.673 0.095 1.660 0.005 2.000 13 8866 0.303
time: 0:00 82:00 0:00 120:00 8866 23:45
Ctrl-Enter = Ready

FIG. 42.

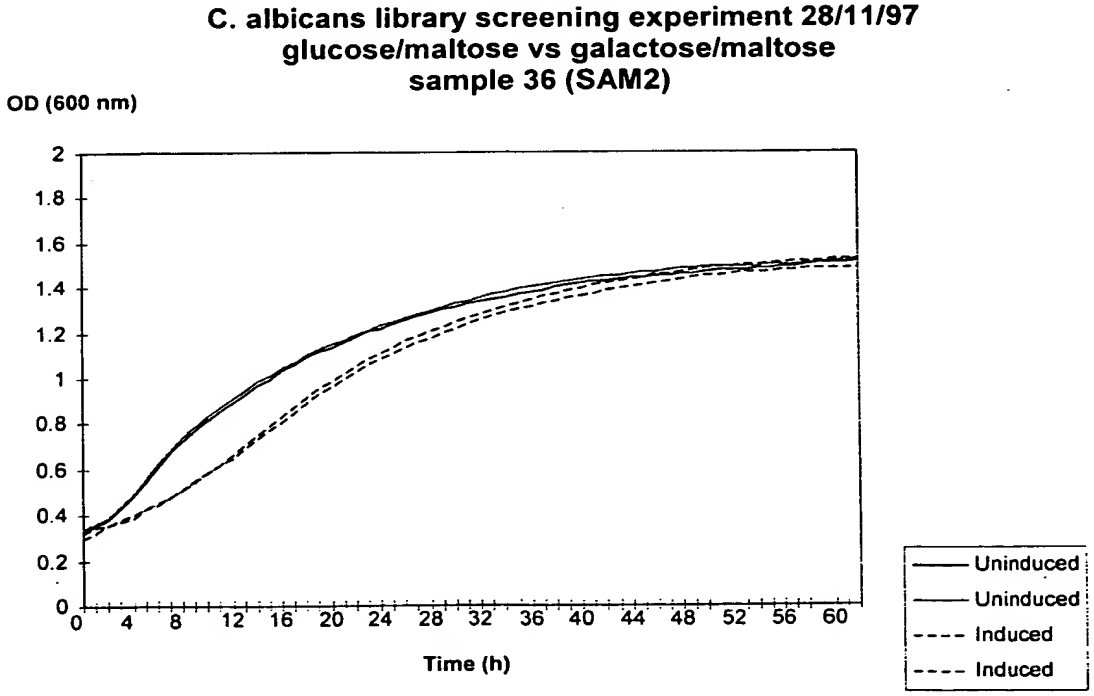

C. albicans library screening experiment 28/11/97
glucose/maltose vs galactose/maltose
sample 36 (SAM2)
OD (600 nm)
2
1.8
1.6
1.4
1.2
1
0.8
0.6
0.4
0.2
0
0 4 8 12 16 20 24 28 32 36 40 44 48 52 56 60
Time (h)
Uninduced
Uninduced
Induced
Induced

FIG. 43.

C. albicans cDNA library screening 05/02/98
glucose/maltose vs galactose/maltose
YPD sample 360

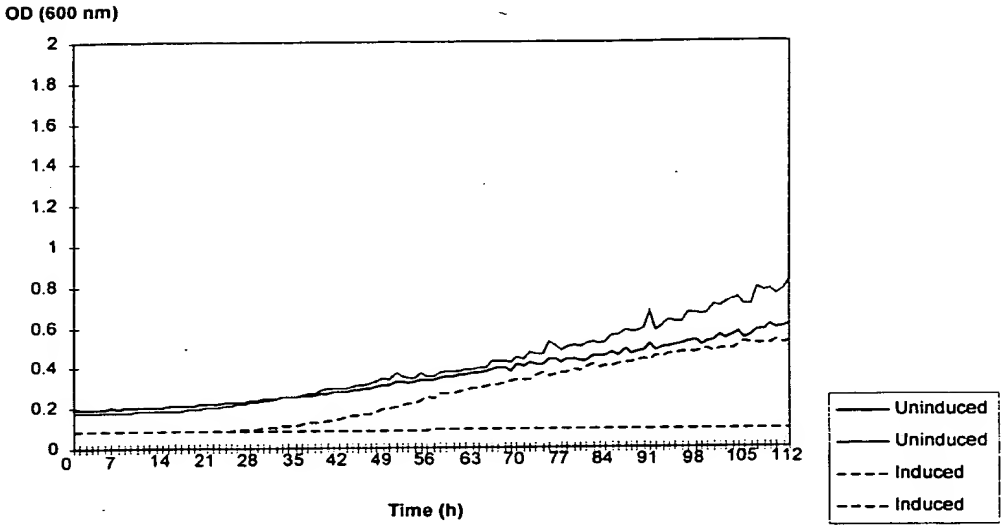


FIG. 44.

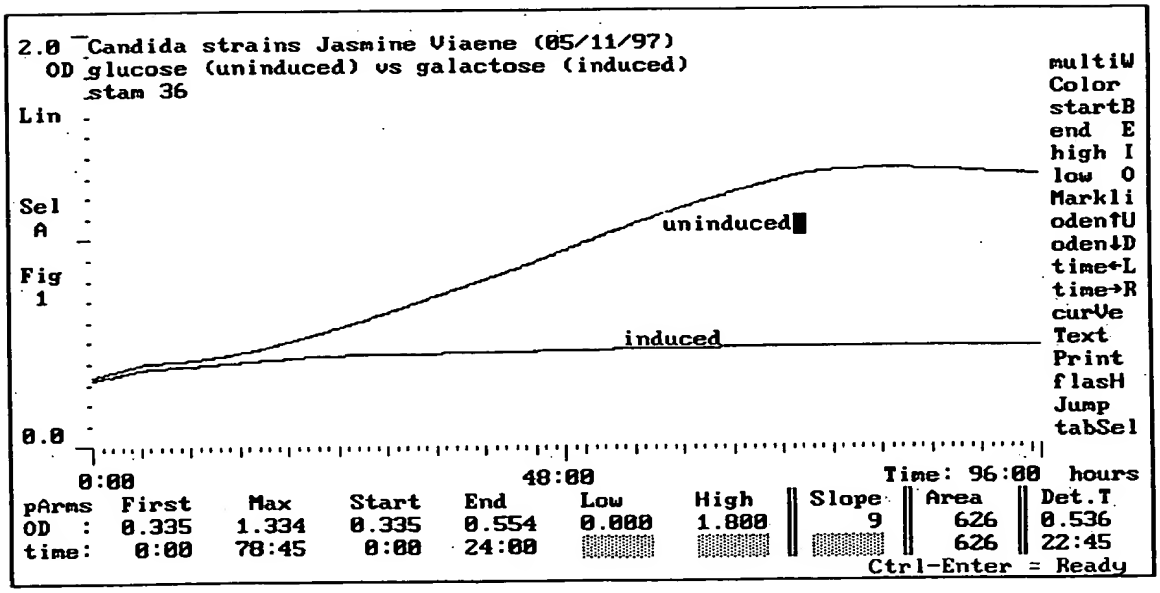


FIG. 45.

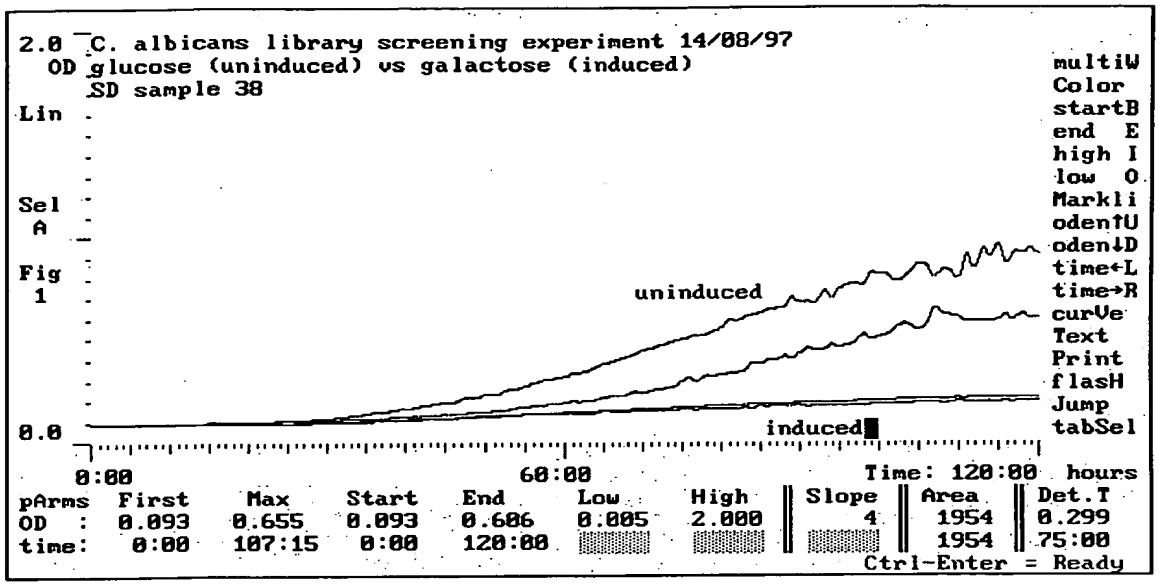

2.0 C. albicans library screening experiment 14/08/97
OD glucose (uninduced) vs galactose (induced)
SD sample 38
Lin
Sel A
Fig 1
uninduced
induced
0.0
0:00
60:00
Time: 120:00 hours
multiW
Color
startB
end E
high I
low O
Markli
odenfU
oden↓D
time←L
time→R
curVe
Text
Print
flasH
Jump
tabSel
pArms First Max Start End Low High Slope Area Det.T
OD : 0.093 0.655 0.093 0.606 0.005 2.000 4 1954 0.299
time: 0:00 107:15 0:00 120:00 1954 75:00
Ctrl-Enter = Ready

FIG. 46.

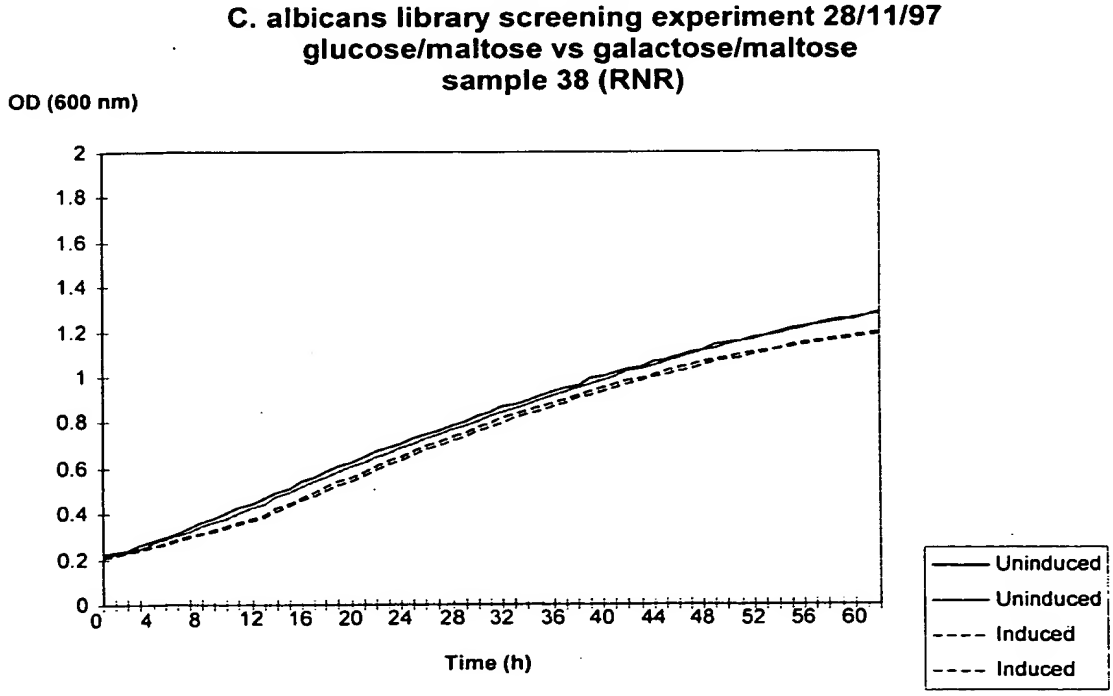
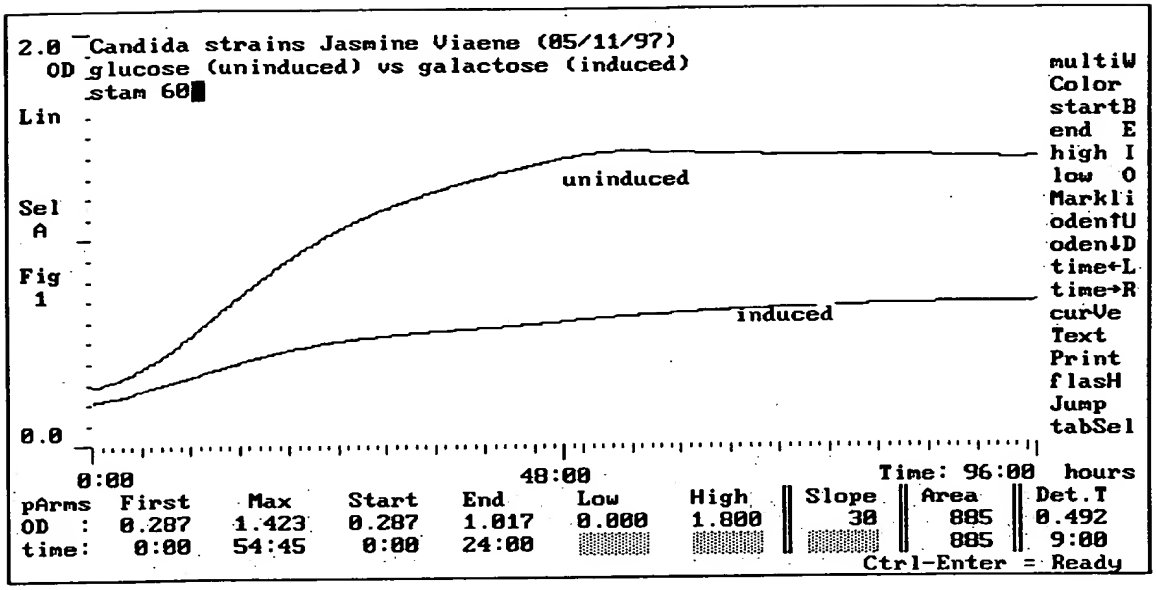

C. albicans library screening experiment 28/11/97
glucose/maltose vs galactose/maltose
sample 38 (RNR)
OD (600 nm)
2
1.8
1.6
1.4
1.2
1
0.8
0.6
0.4
0.2
0
0 4 8 12 16 20 24 28 32 36 40 44 48 52 56 60
Time (h)
Uninduced
Uninduced
Induced
Induced

FIG. 47.



60gK (RAD18)

FIG. 48.

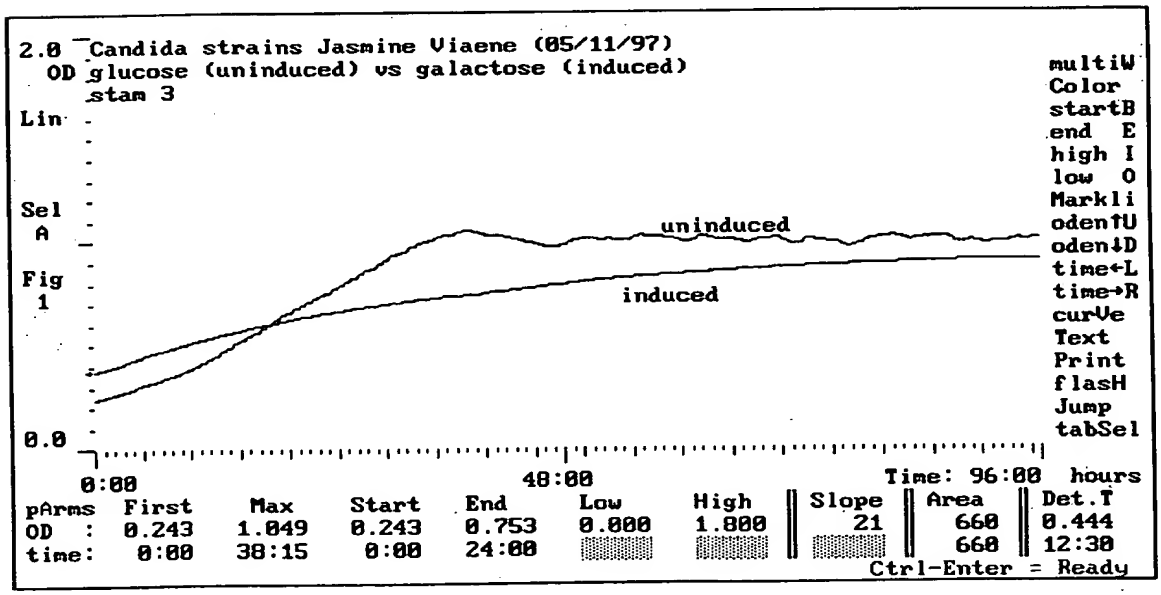


FIG. 49.

C. albicans cDNA library screening 12-02-98
glucose/maltose vs galactose/maltose
YPD sample 409

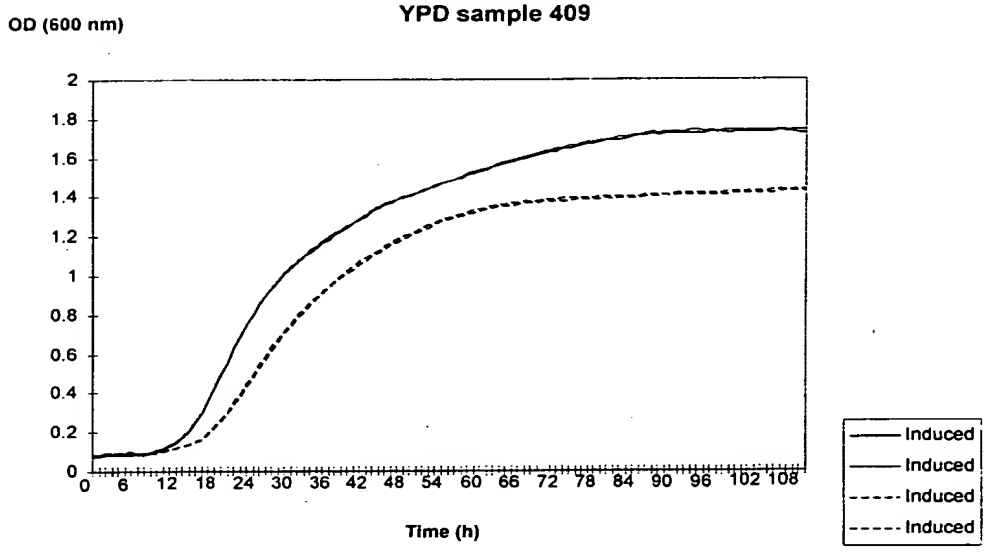


FIG. 50.

C. albicans library screening experiment 27/03/98
glucose/maltose vs galactose/maltose
sample 40AF

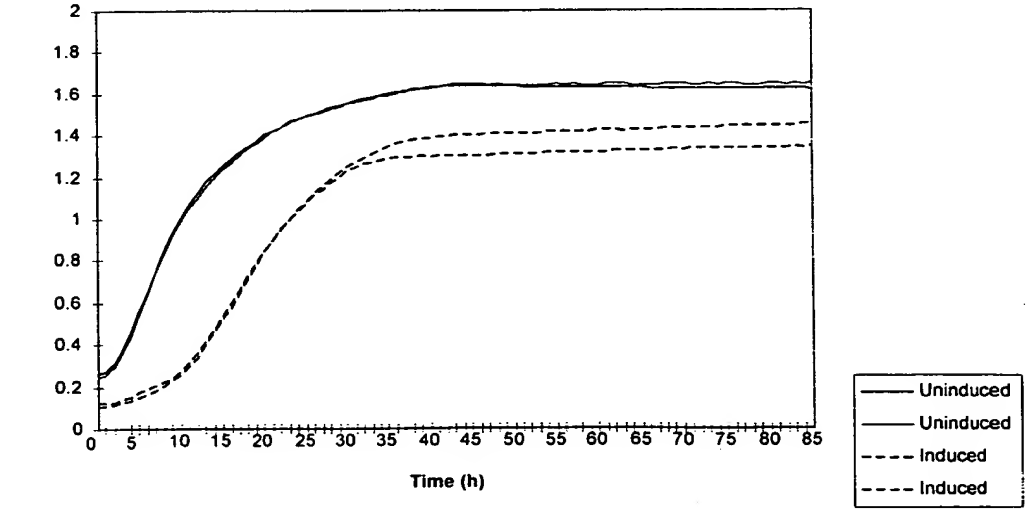


FIG. 51.

C. albicans library screening experiment 17/03/98
glucose/maltose vs galactose/maltose
SD sample 485c

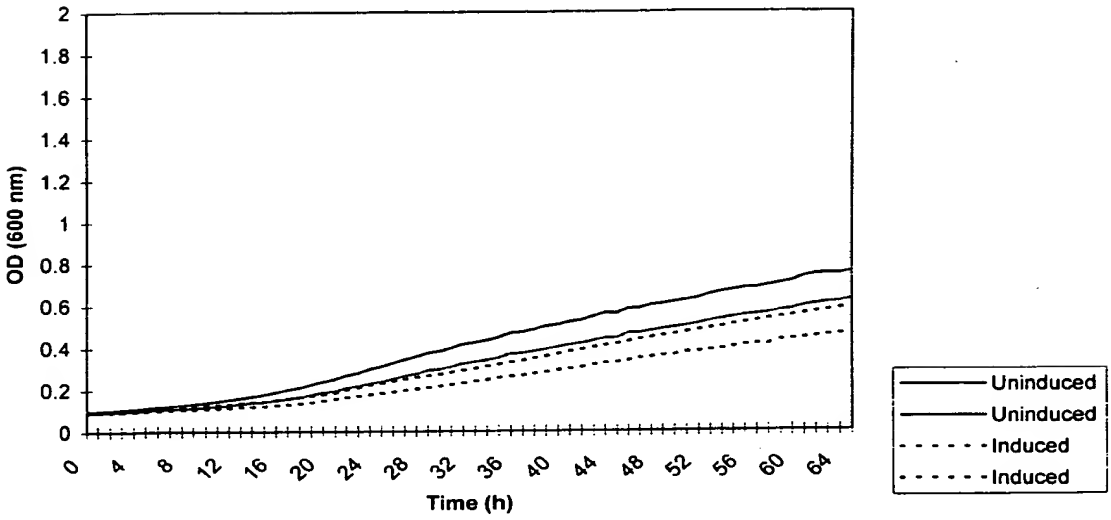


FIG. 52.

C. albicans cDNA library screening 10-03-98
glucose vs galactose
SD sample 480c

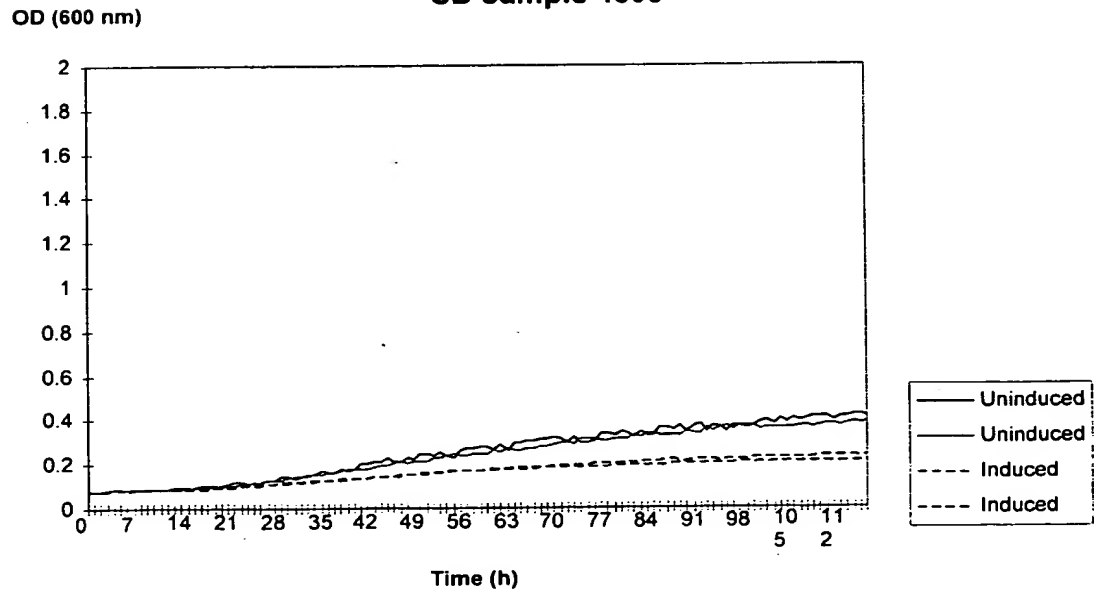
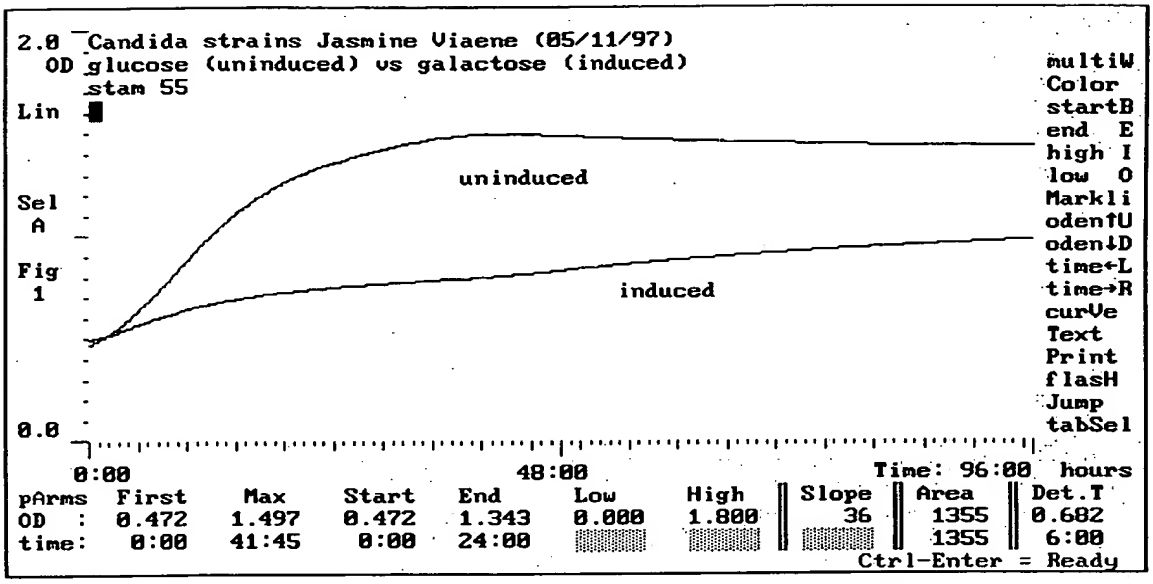


FIG.53.

(a)


2.0 Candida strains Jasmine Vlaene (05/11/97)
OD glucose (uninduced) vs galactose (induced)
stam 55
Lin
Sel A
Fig 1
uninduced
induced
0.0
0:00
48:00
Time: 96:00 hours
multiW
Color
startB
end E
high I
low O
Markli
odenUU
odenDD
time←L
time→R
curVe
Text
Print
flasH
Jump
tabSel
pArms First Max Start End Low High Slope Area Det.T
OD : 0.472 1.497 0.472 1.343 0.000 1.800 36 1355 0.682
time: 0:00 41:45 0:00 24:00 1355 6:00
Ctrl-Enter = Ready

(b)

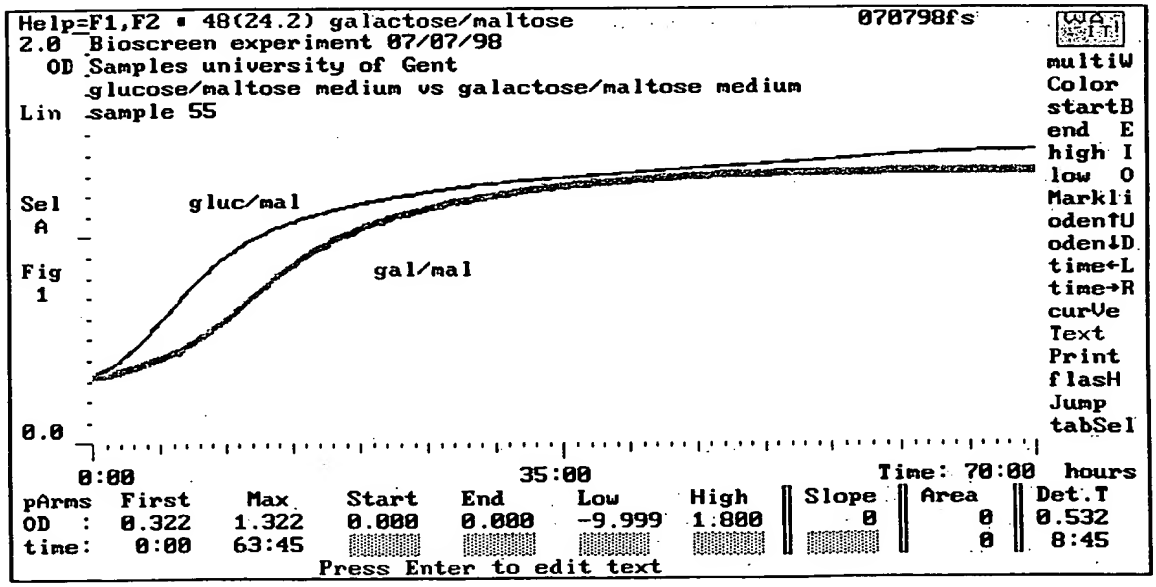

Help=F1,F2 ▪ 48(24.2) galactose/maltose
070798fs
2.0 Bioscreen experiment 07/07/98
OD Samples university of Gent
glucose/maltose medium vs galactose/maltose medium
Lin sample 55
Sel A
Fig 1
gluc/mal
gal/mal
0.0
0:00
35:00
Time: 70:00 hours
multiW
Color
startB
end E
high I
low O
Markli
odenUU
odenDD
time←L
time→R
curVe
Text
Print
flasH
Jump
tabSel
pArms First Max Start End Low High Slope Area Det.T
OD : 0.322 1.322 0.000 0.000 -9.999 1.800 0 0 0.532
time: 0:00 63:45 0 0 8:45
Press Enter to edit text

FIG. 54.

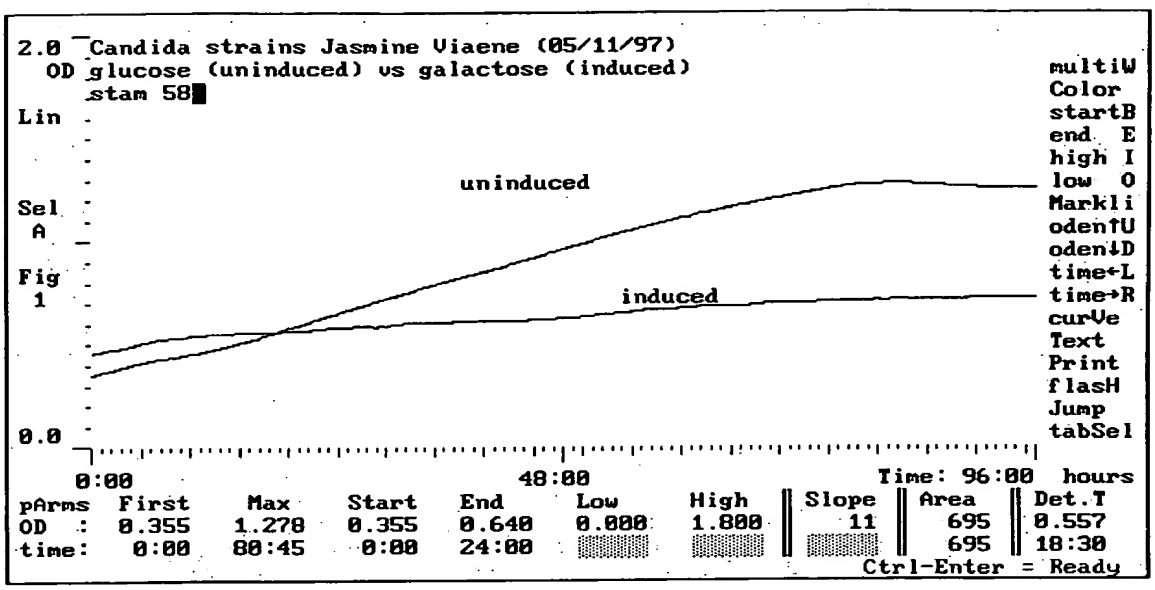


FIG. 55.

C. albicans library screening experiment 31/03/98
glucose/maltose vs galactose/maltose
sample 8CP

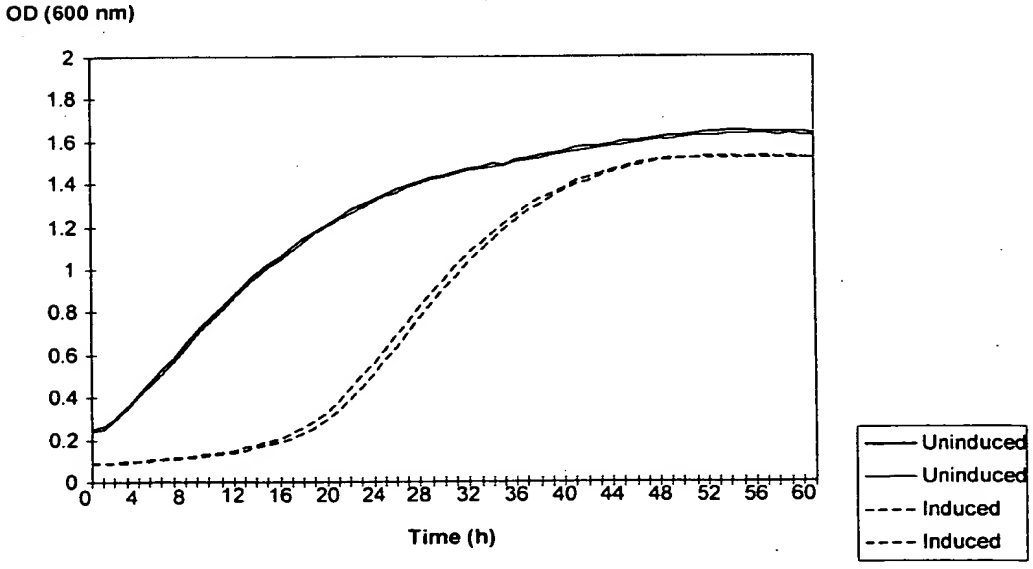


FIG. 56.

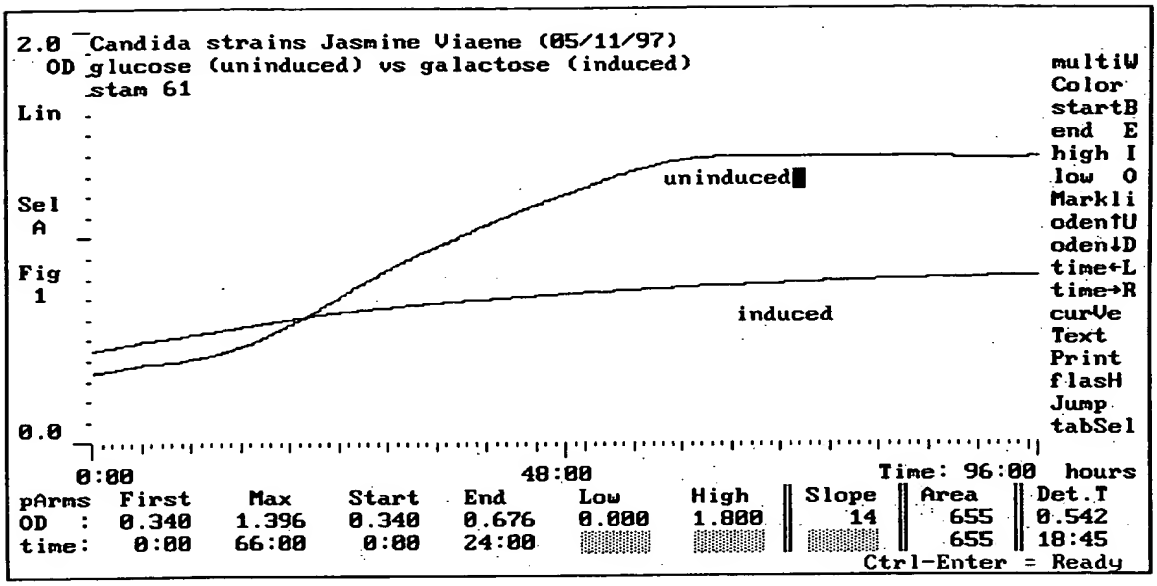

2.0 Candida strains Jasmine Viaene (05/11/97)
OD glucose (uninduced) vs galactose (induced)
stam 61
Lin
Sel
A
Fig
1
0.0
uninduced
induced
multiW
Color
startB
end E
high I
low O
Markli
odenUU
odenDD
timeLL
timeRR
curVe
Text
Print
flasH
Jump
tabSel
0:00
48:00
Time: 96:00 hours
pArms First Max Start End Low High Slope Area Det.T
OD : 0.340 1.396 0.340 0.676 0.000 1.800 14 655 0.542
time: 0:00 66:00 0:00 24:00 655 18:45
Ctrl-Enter = Ready

FIG. 57.

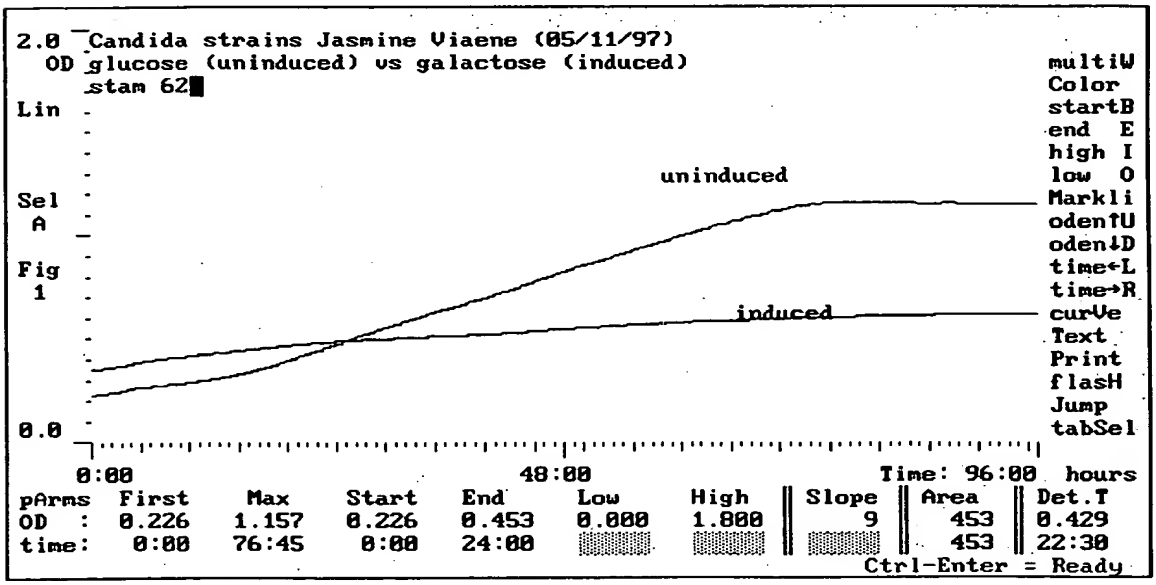

2.0 Candida strains Jasmine Viaene (05/11/97)
OD glucose (uninduced) vs galactose (induced)
stam 62
Lin
Sel
A
Fig
1
0.0
uninduced
induced
multiW
Color
startB
end E
high I
low O
Markli
odenUU
odenDD
timeLL
timeRR
curVe
Text
Print
flasH
Jump
tabSel
0:00
48:00
Time: 96:00 hours
pArms First Max Start End Low High Slope Area Det.T
OD : 0.226 1.157 0.226 0.453 0.000 1.800 9 453 0.429
time: 0:00 76:45 0:00 24:00 453 22:30
Ctrl-Enter = Ready

FIG. 58.

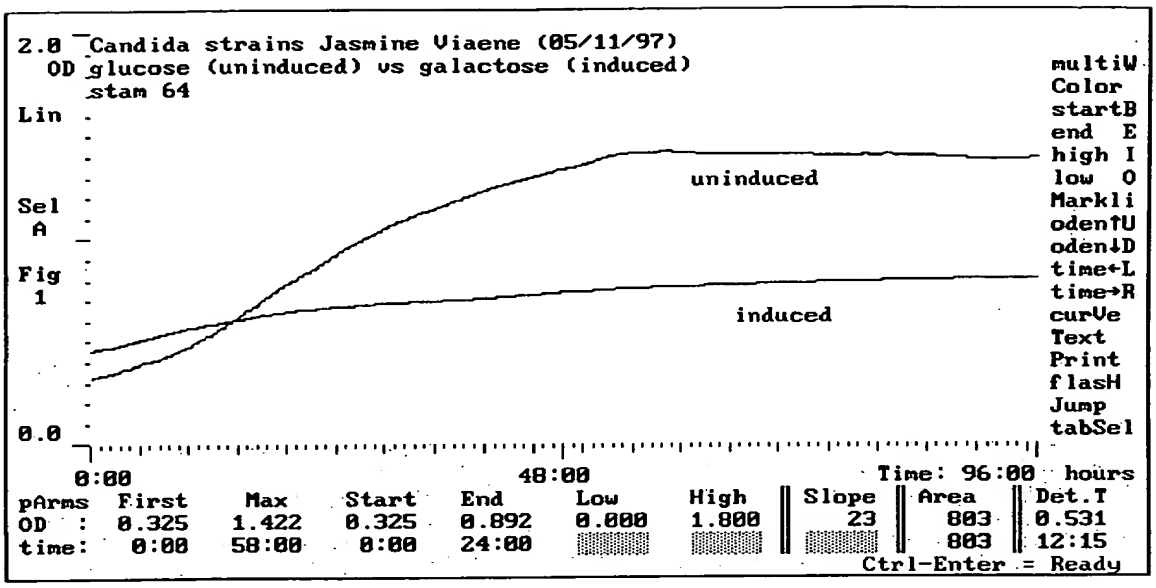

2.0
OD
Lin
Sel
A
Fig
1
0.0
Candida strains Jasmine Viaene (05/11/97)
glucose (uninduced) vs galactose (induced)
stam 64
uninduced
induced
multiW
Color
startB
end E
high I
low O
Markli
odenUp
odenDn
timeLft
timeRt
curVe
Text
Print
flasH
Jump
tabSel
0:00
48:00
Time: 96:00 hours
pArms First Max Start End Low High Slope Area Det.T
OD : 0.325 1.422 0.325 0.892 0.000 1.800 23 803 0.531
time: 0:00 58:00 0:00 24:00 803 12:15
Ctrl-Enter = Ready

FIG. 59.

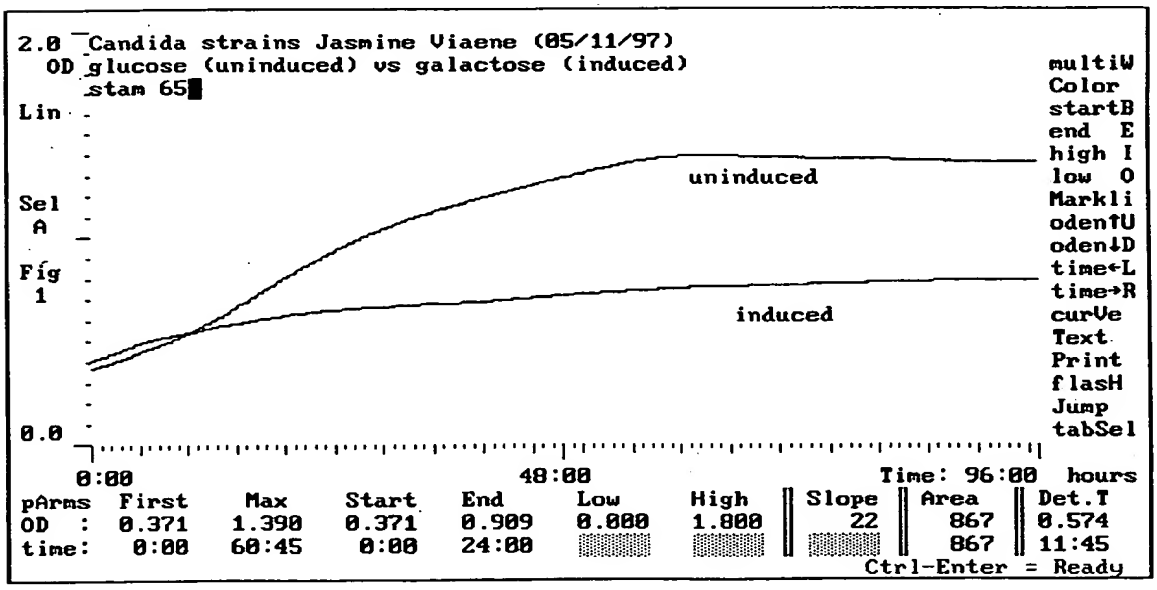

2.0
OD
Lin
Sel
A
Fig
1
0.0
Candida strains Jasmine Viaene (05/11/97)
glucose (uninduced) vs galactose (induced)
stam 65
uninduced
induced
multiW
Color
startB
end E
high I
low O
Markli
odenUp
odenDn
timeLft
timeRt
curVe
Text
Print
flasH
Jump
tabSel
0:00
48:00
Time: 96:00 hours
pArms First Max Start End Low High Slope Area Det.T
OD : 0.371 1.390 0.371 0.909 0.000 1.800 22 867 0.574
time: 0:00 60:45 0:00 24:00 867 11:45
Ctrl-Enter = Ready

FIG. 60.

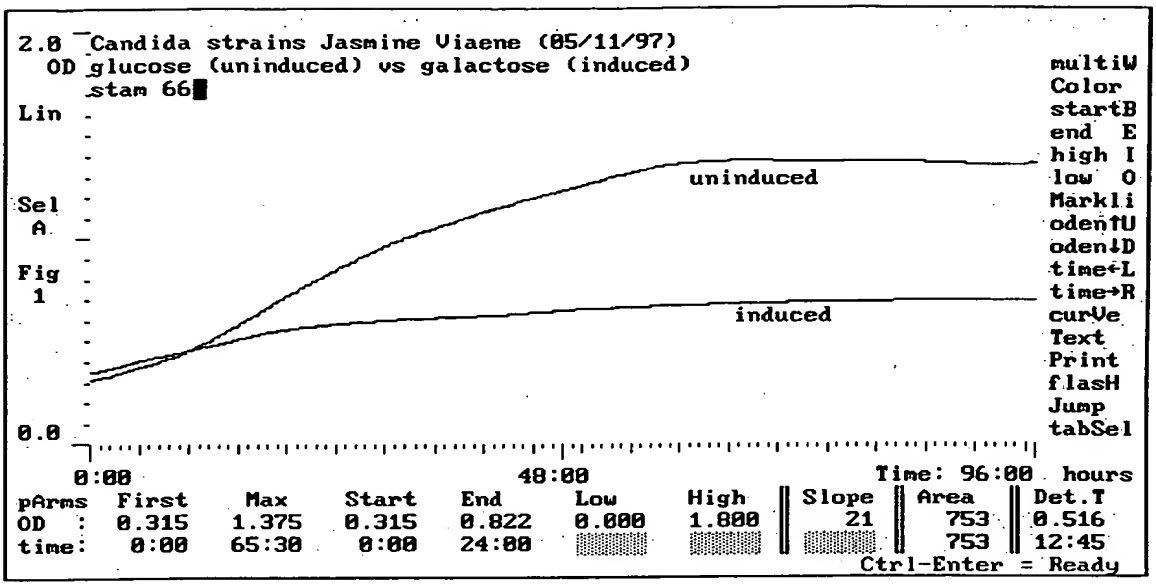

2.0 Candida strains Jasmine Viaene (05/11/97)
OD glucose (uninduced) vs galactose (induced)
stam 66
Lin
Sel A
Fig 1
0.0
uninduced
induced
multiW
Color
startB
end E
high I
low O
Markli
odenfU
oden↓D
time←L
time→R
curVe
Text
Print
flasH
Jump
tabSel
0:00
48:00
Time: 96:00 hours
pArms First Max Start End Low High Slope Area Det.T
OD : 0.315 1.375 0.315 0.822 0.000 1.000 21 753 0.516
time: 0:00 65:30 0:00 24:00 753 12:45
Ctrl-Enter = Ready

FIG. 61.

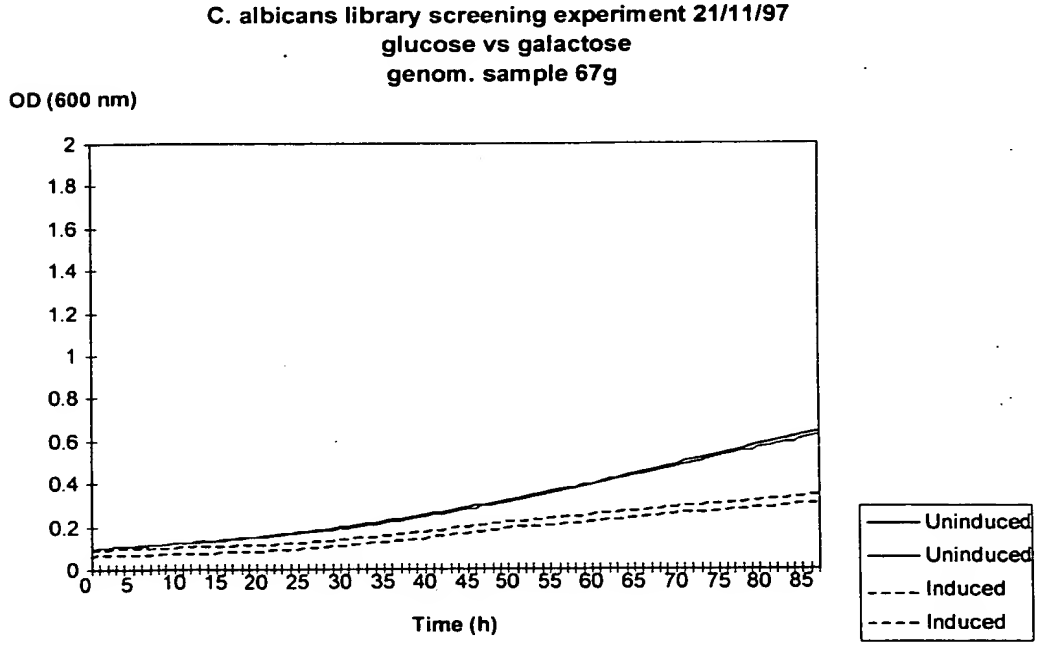

C. albicans library screening experiment 21/11/97
glucose vs galactose
genom. sample 67g
OD (600 nm)
2
1.8
1.6
1.4
1.2
1
0.8
0.6
0.4
0.2
0
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85
Time (h)
Uninduced
Uninduced
Induced
Induced

FIG. 62.

C. albicans library screening experiment 21/11/97
glucose vs galactose
genom. sample 80g

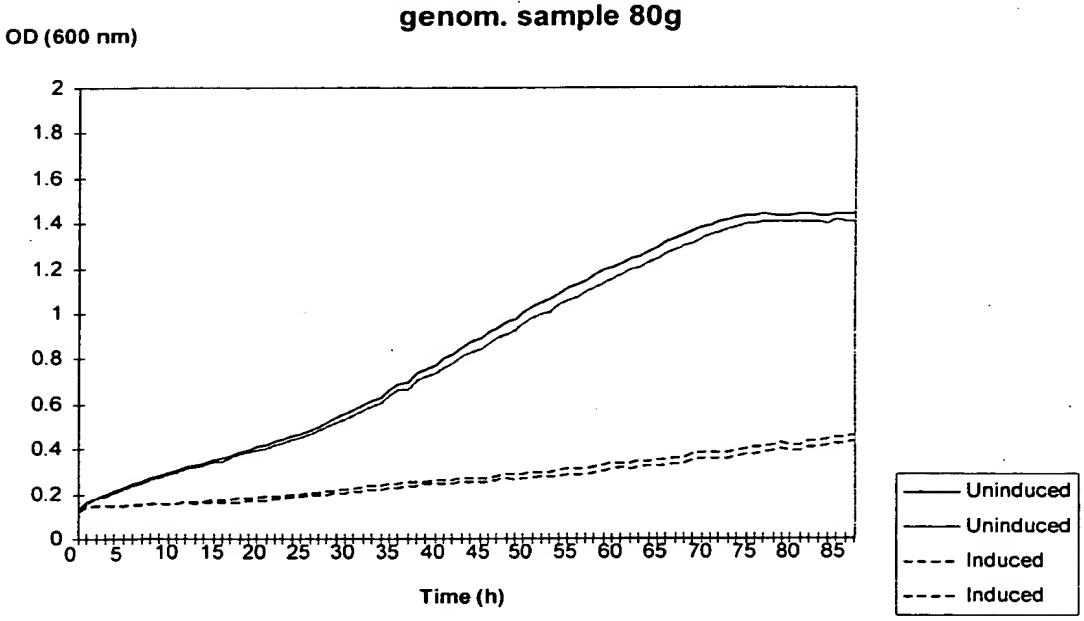


FIG. 63.

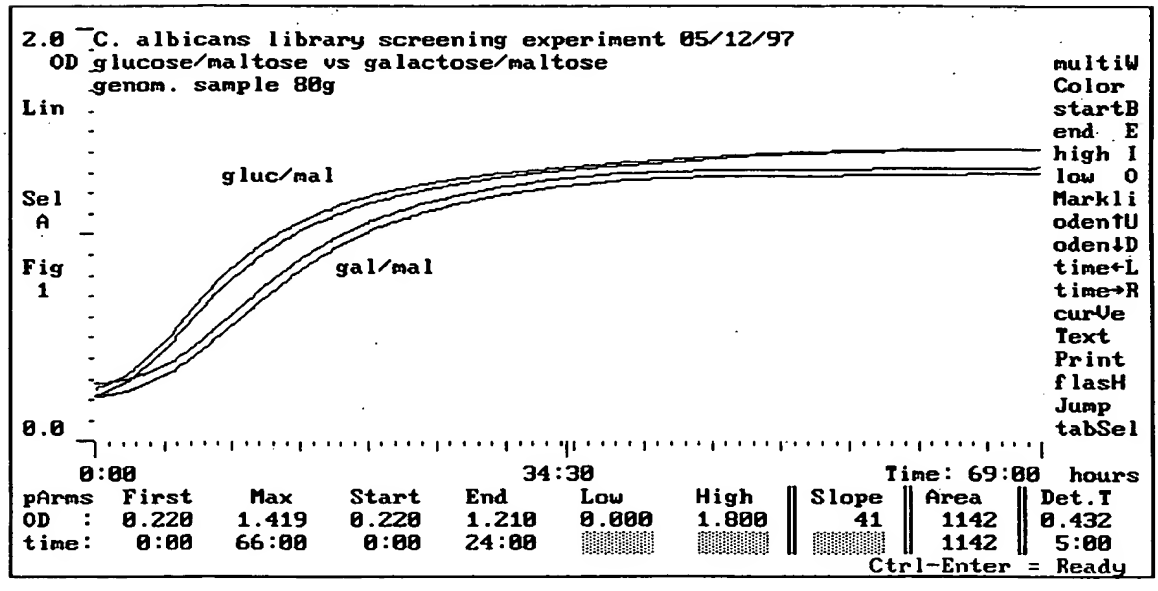
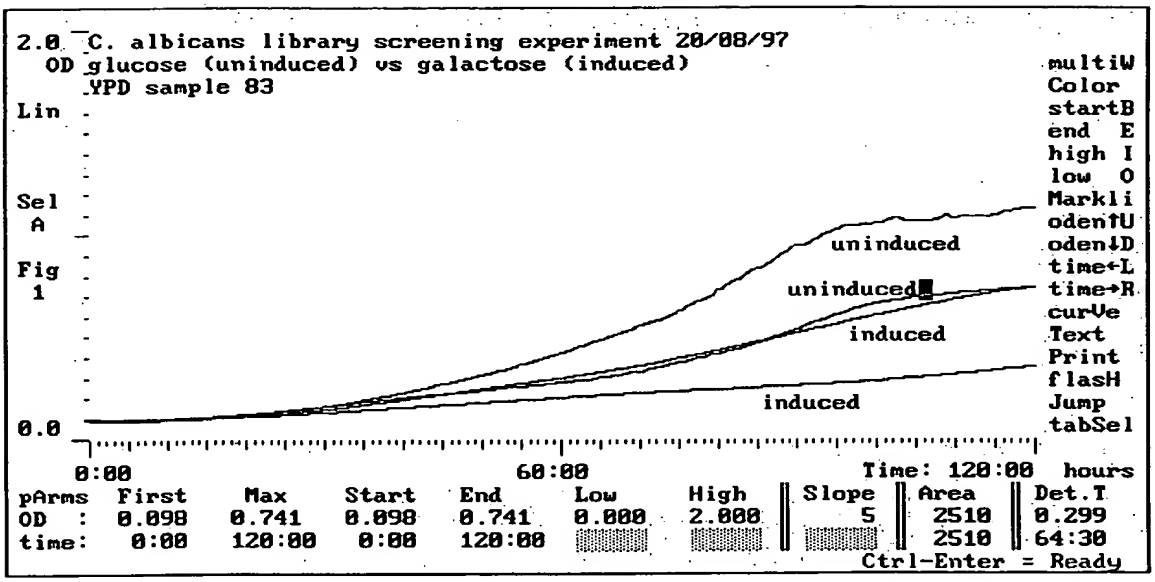


FIG. 64.



83c3 (SHA3)

FIG. 65.

C. albicans library screening experiment 21/11/97
glucose vs galactose
genom. sample 85g

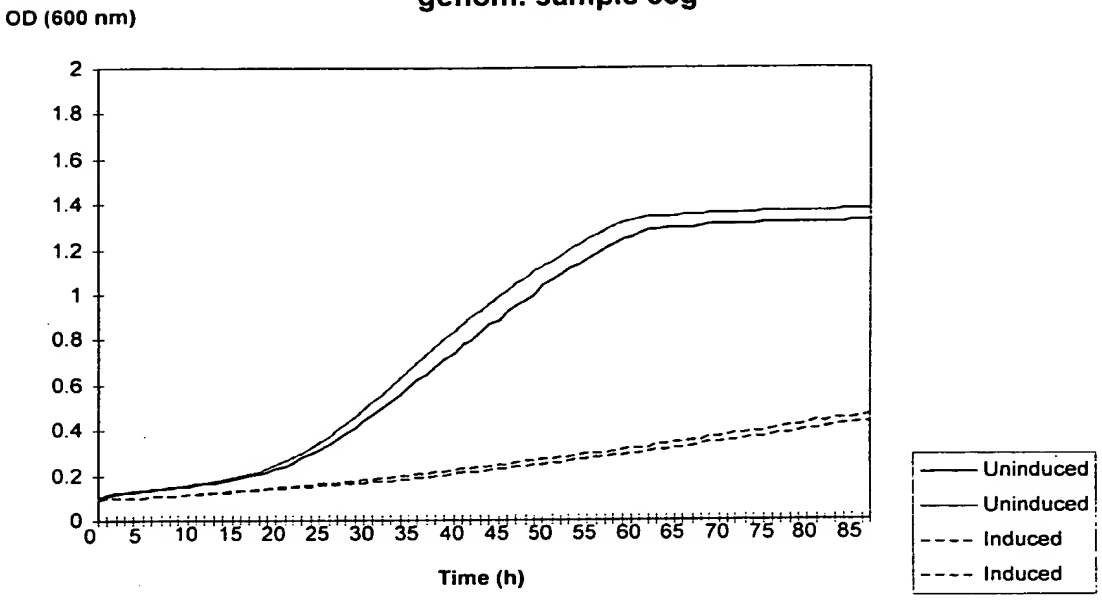


FIG. 66.

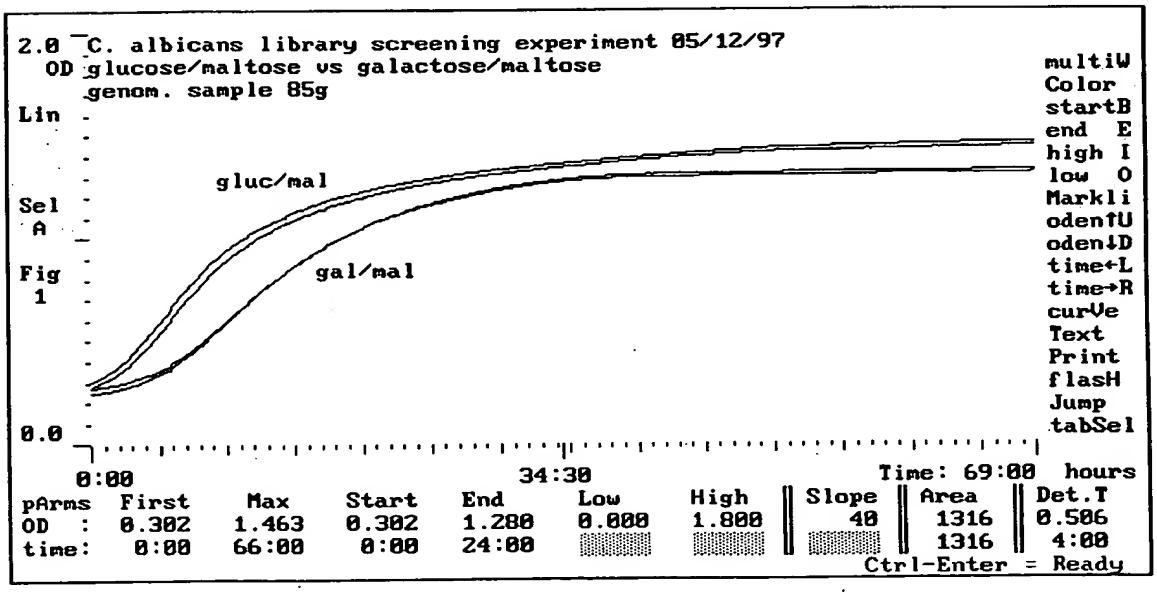


FIG. 67.

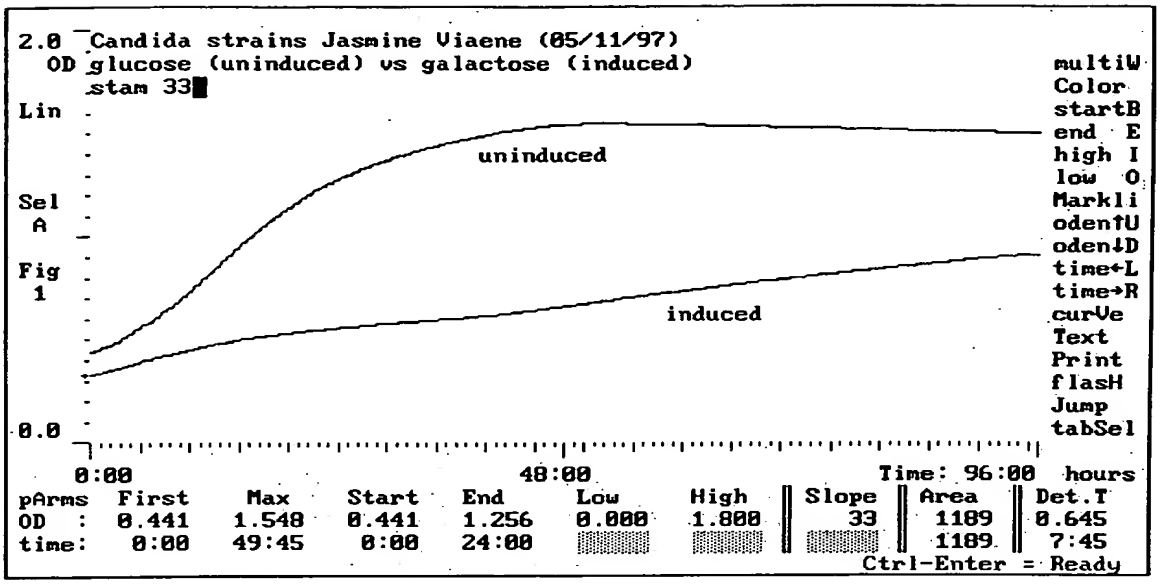
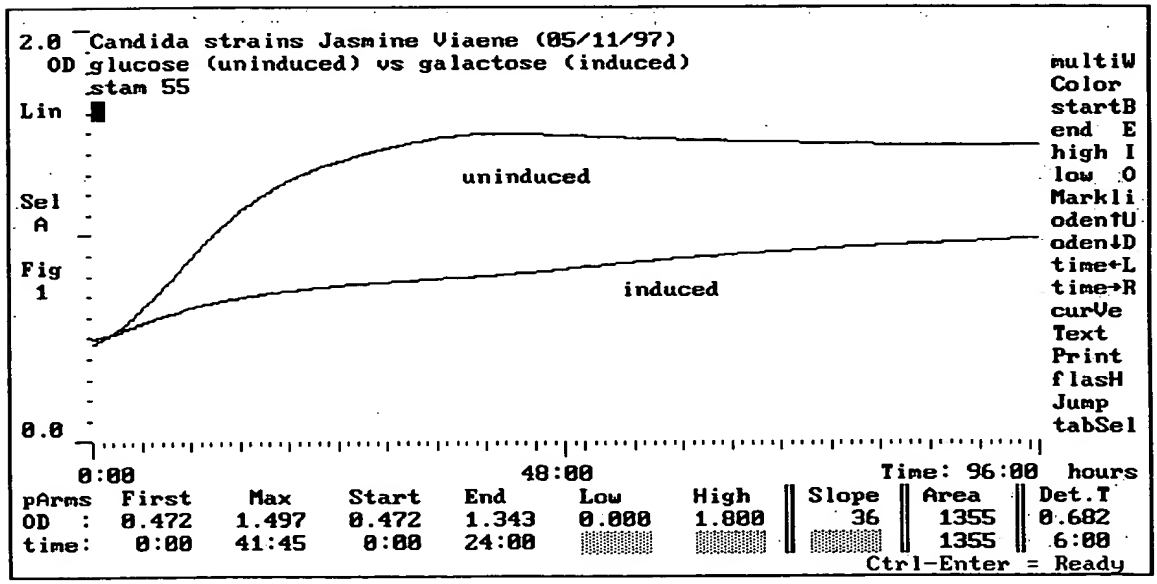

2.0 Candida strains Jasmine Viaene (05/11/97)
OD glucose (uninduced) vs galactose (induced)
stam 33
Lin
Sel A
Fig 1
0.0
uninduced
induced
0:00
48:00
Time: 96:00 hours
multiW
Color
startB
end E
high I
low O
Markli
odenUU
odenDD
timeLL
timeRR
curVe
Text
Print
flasH
Jump
tabSel
pArms First Max Start End Low High Slope Area Det.T
OD : 0.441 1.548 0.441 1.256 0.000 1.800 33 1189 0.645
time: 0:00 49:45 0:00 24:00 1189 7:45
Ctrl-Enter = Ready

FIG. 68.


2.0 Candida strains Jasmine Viaene (05/11/97)
OD glucose (uninduced) vs galactose (induced)
stam 55
Lin
Sel A
Fig 1
0.0
uninduced
induced
0:00
48:00
Time: 96:00 hours
multiW
Color
startB
end E
high I
low O
Markli
odenUU
odenDD
timeLL
timeRR
curVe
Text
Print
flasH
Jump
tabSel
pArms First Max Start End Low High Slope Area Det.T
OD : 0.472 1.497 0.472 1.343 0.000 1.800 36 1355 0.682
time: 0:00 41:45 0:00 24:00 1355 6:00
Ctrl-Enter = Ready

63/75

FIG. 69.

C. albicans library screening experiment 21/11/97
glucose vs galactose
genom. sample 99g

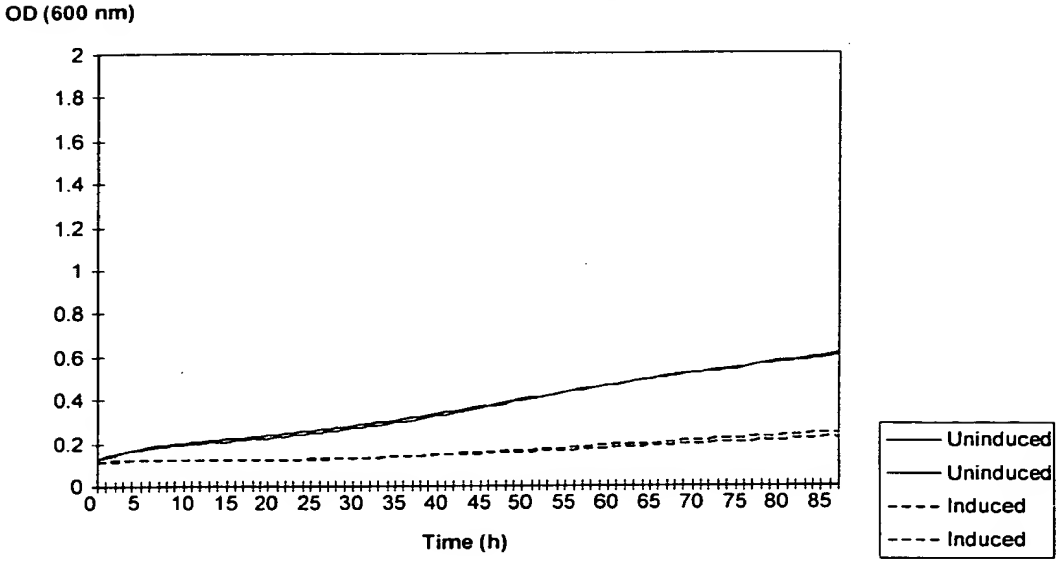


FIG. 70.

C. albicans library screening experiment 24/04/98
glucose/maltose vs galactose/maltose
sample 98cp

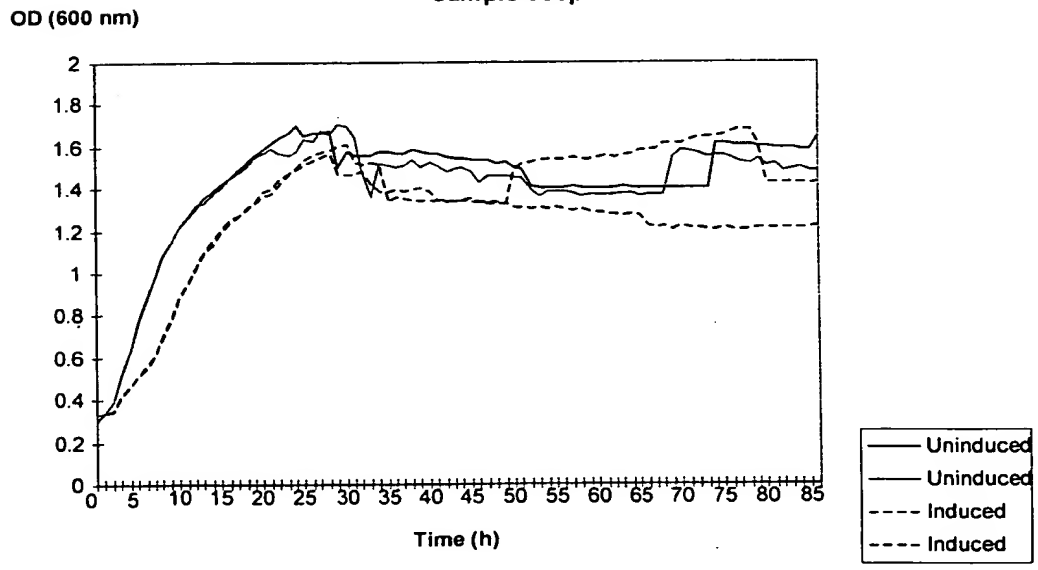


FIG. 7I

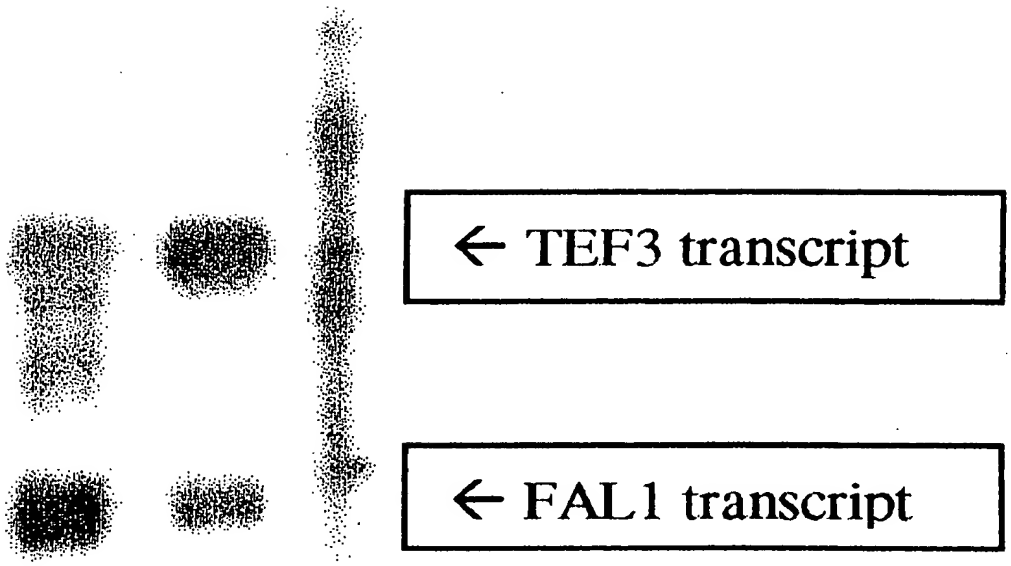
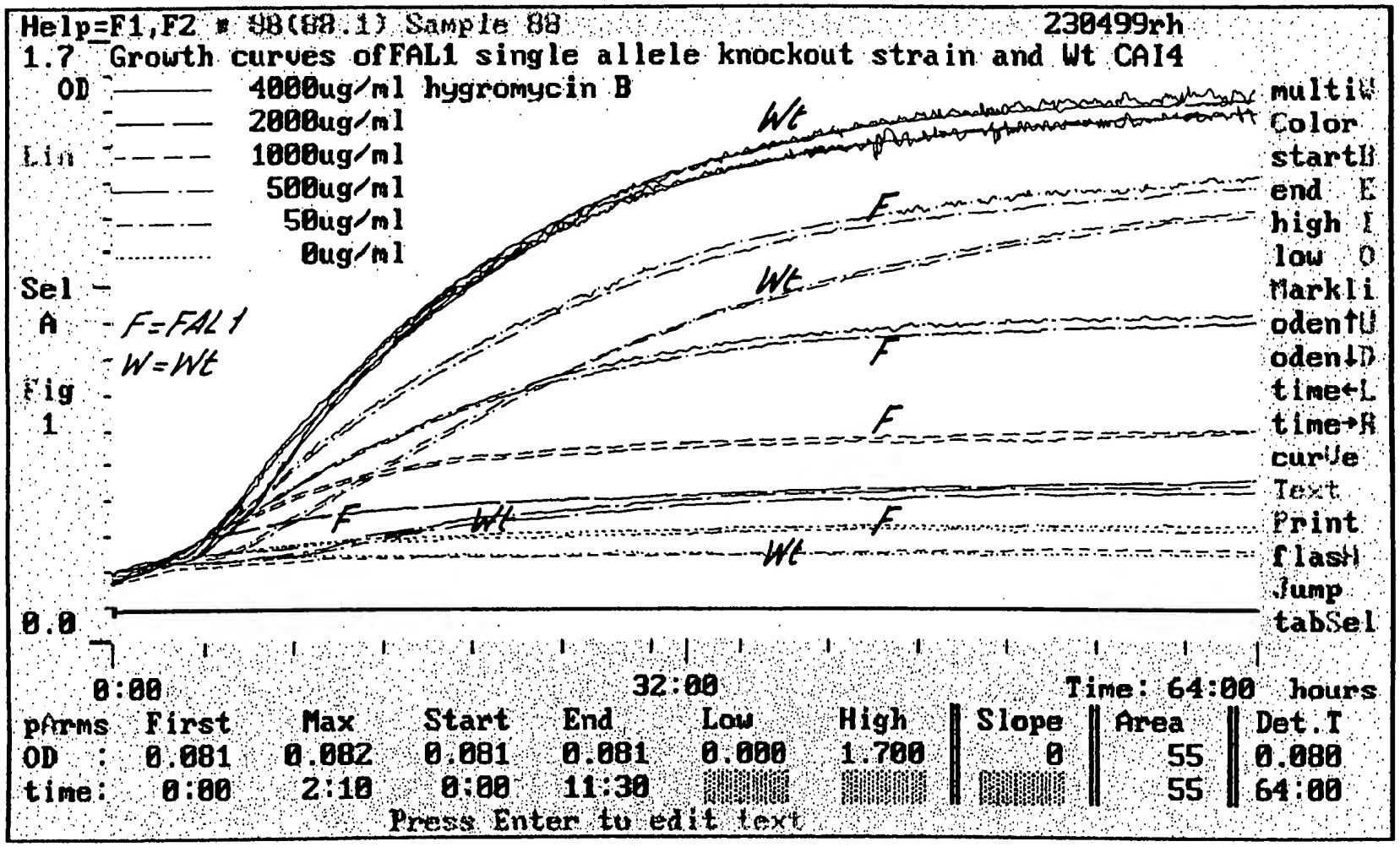
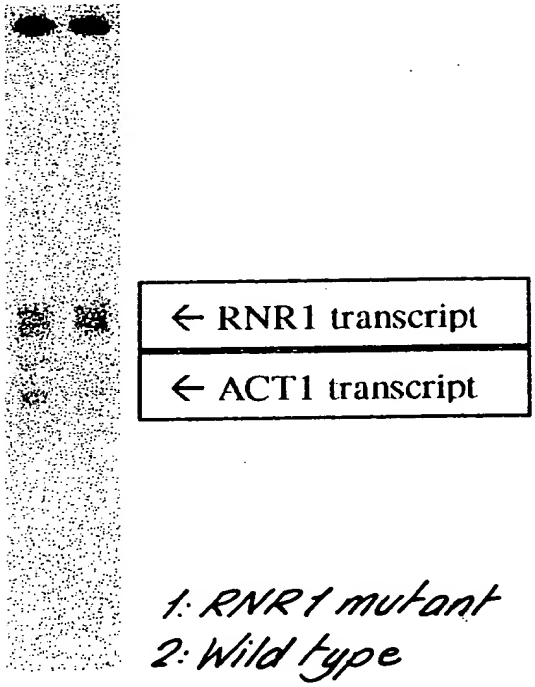


FIG. 72.



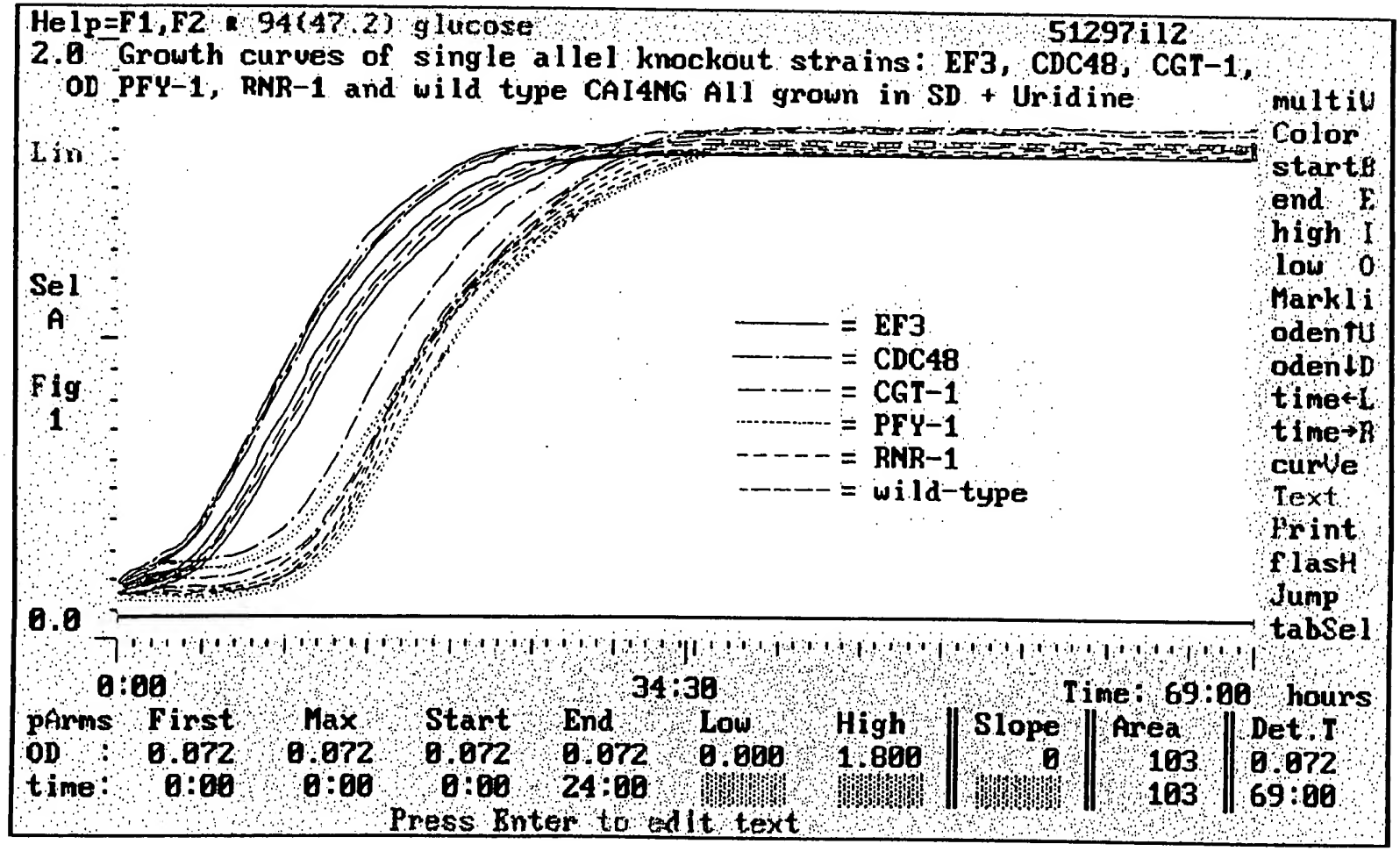
The FAL1 single allele knock-out grows equal to the wild type, however it is significantly more resistant to Hygromycin B.

FIG. 73.



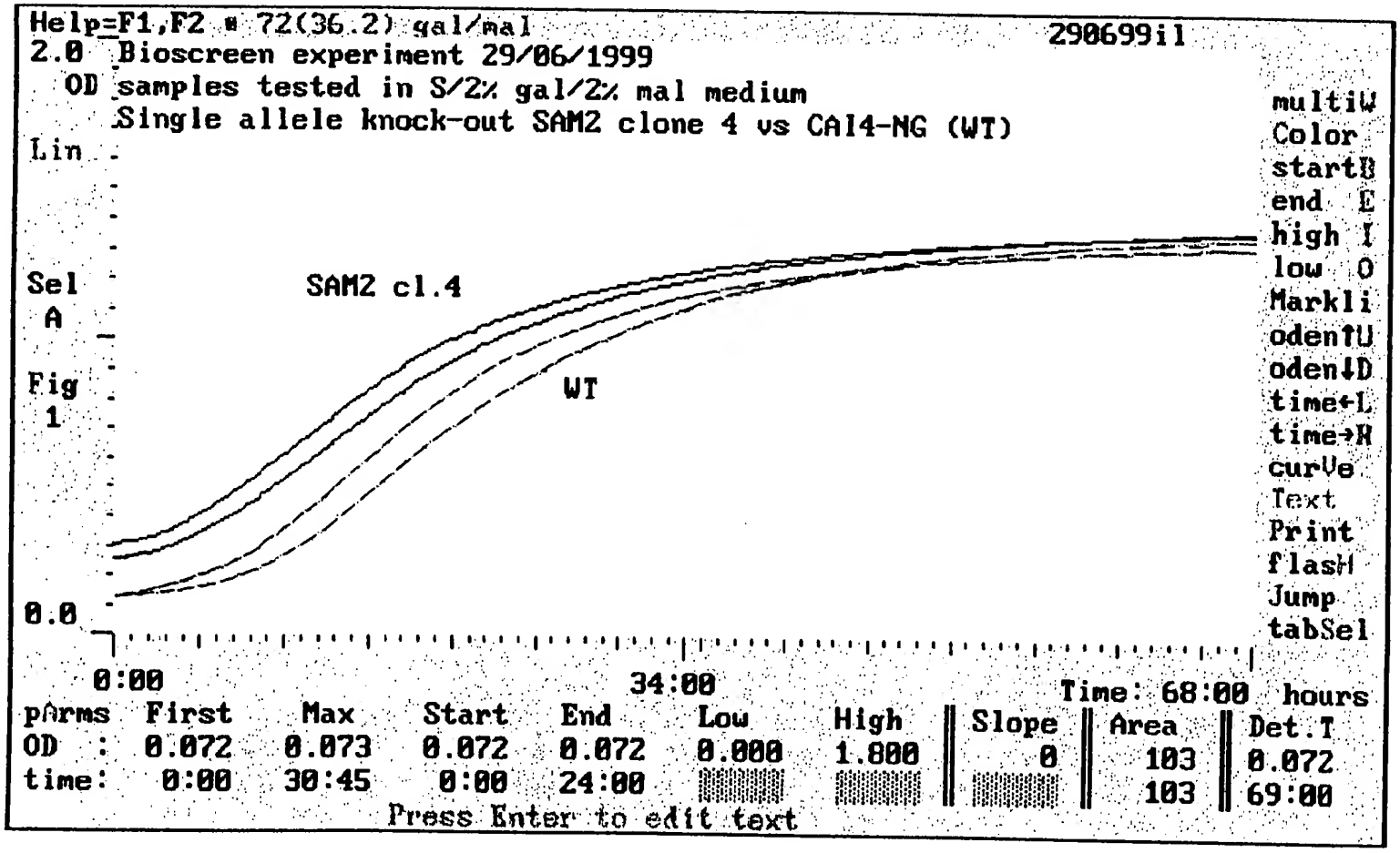
1: RNR1 mutant
2: Wild type

FIG. 74.



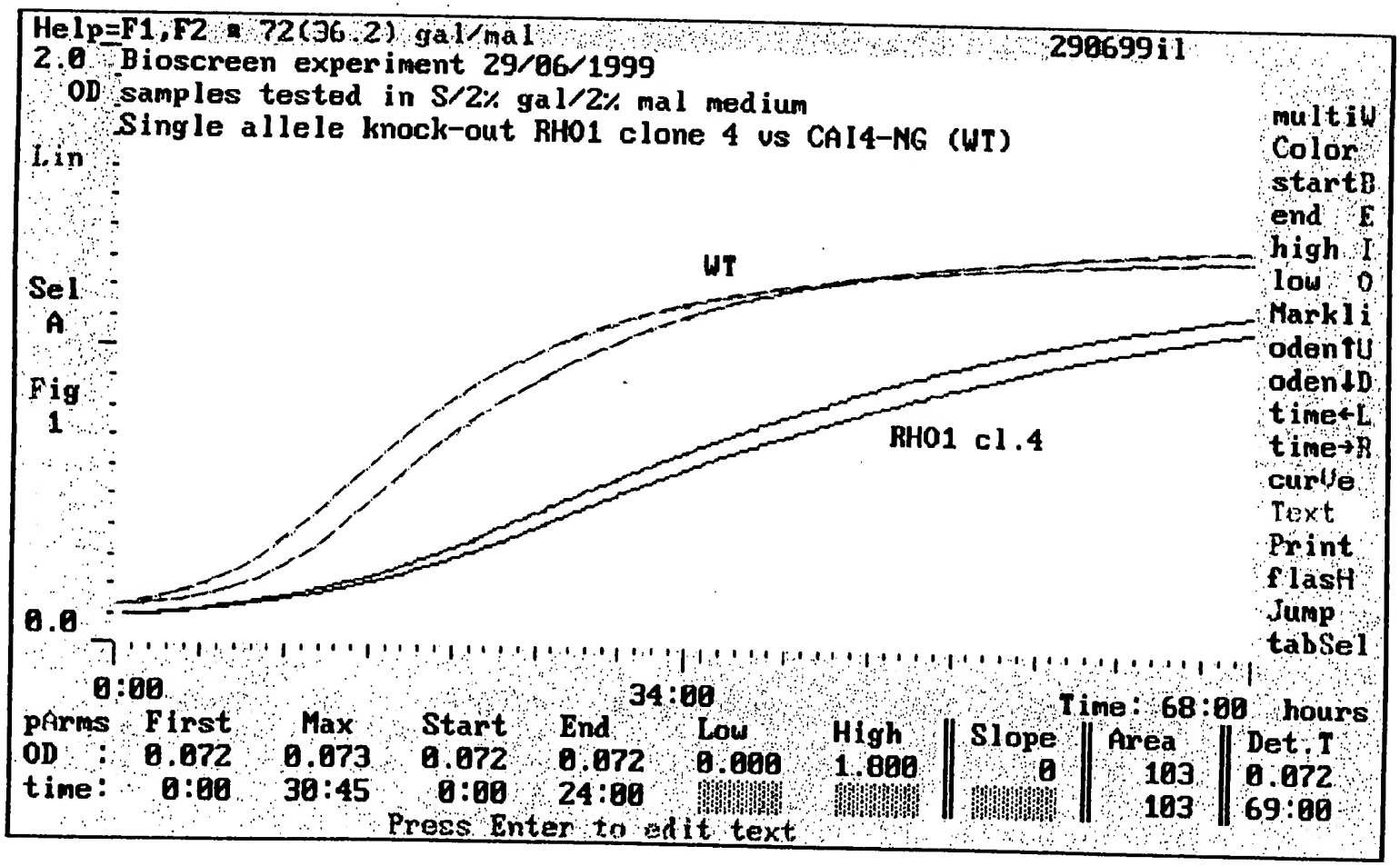
The RNR1 single allele knock-out shows an extended LAG phase compared to the wild type.

FIG 75



Inoculum for SAM2 was somewhat higher; at equal inocula growth of SAM2 single allele knock-out is slightly slower.

FIG. 76.

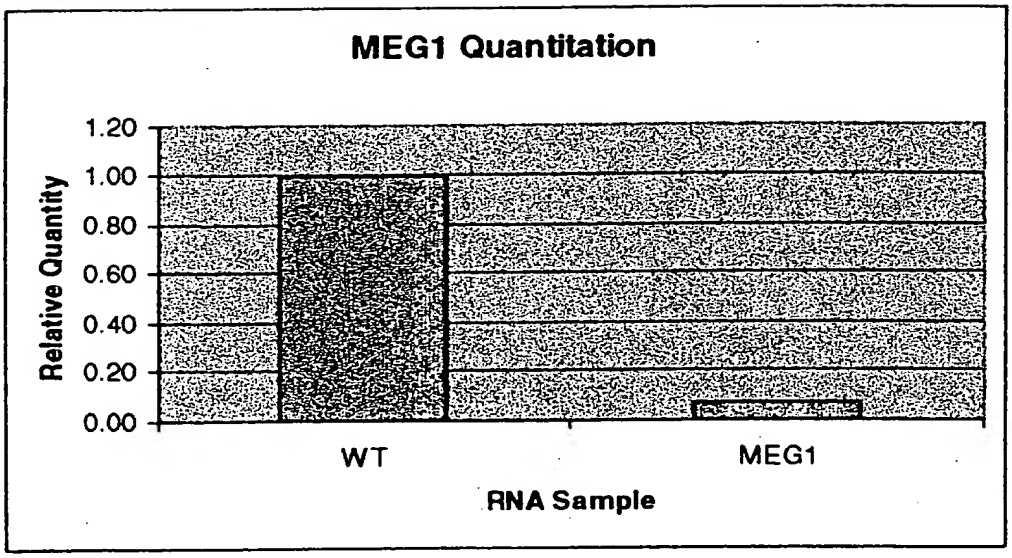


Growth of the RHO1 single allele knock-out is impaired compared to wild type growth.

FIG. 77.

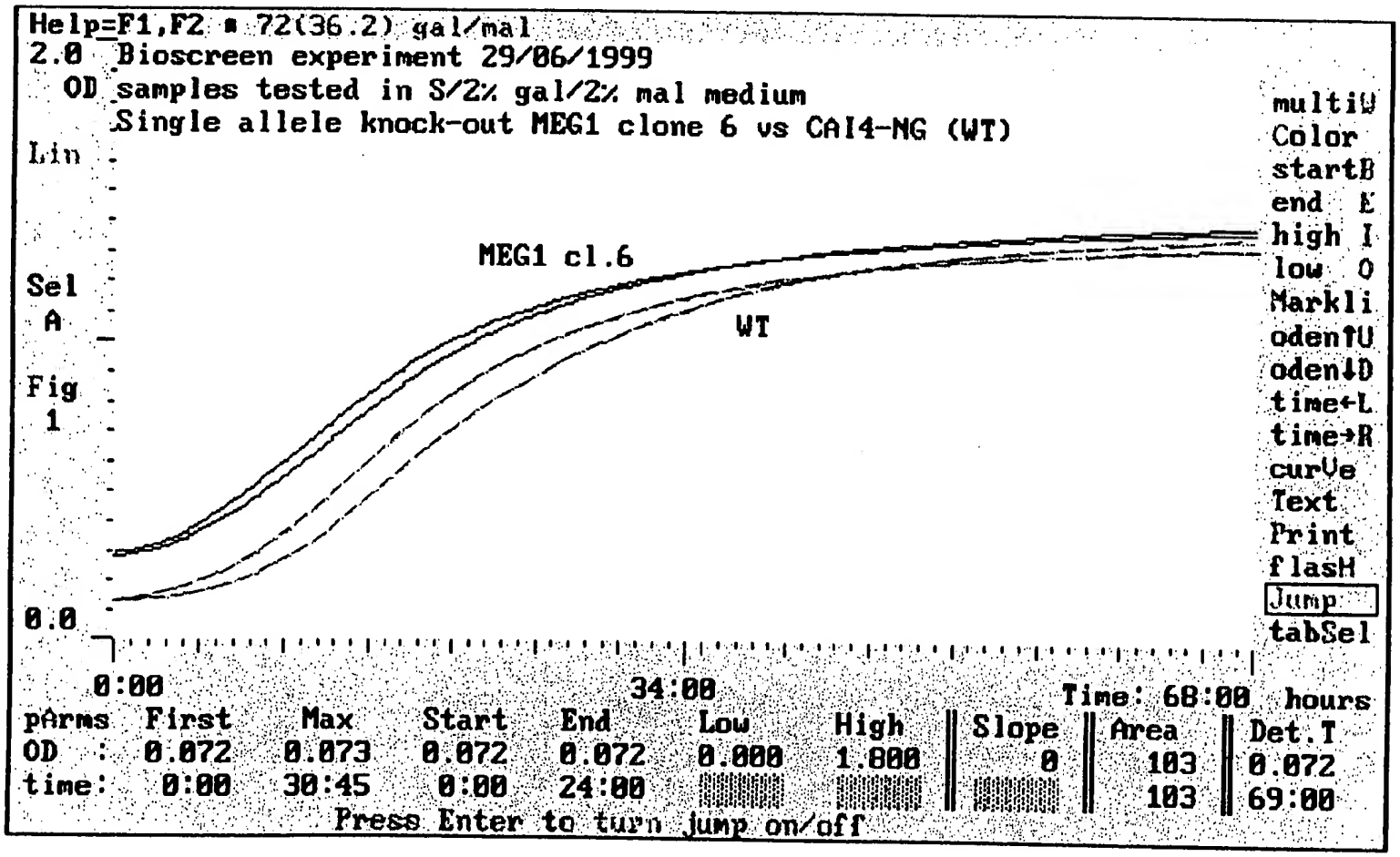
Relative quantitation for MEG1 vs. Act

	Avrg. MEG1	Avrg. ACT	dCt	ddCt	2-ddct
WT	35.79	33.49	2.29	0.00	1.00
MEG1	38.62	32.57	6.05	3.76	0.07



MEG1 expression was decreased more than 14 fold in the MEG1 single allele knock- out compared to the Wt.

FIG. 78.

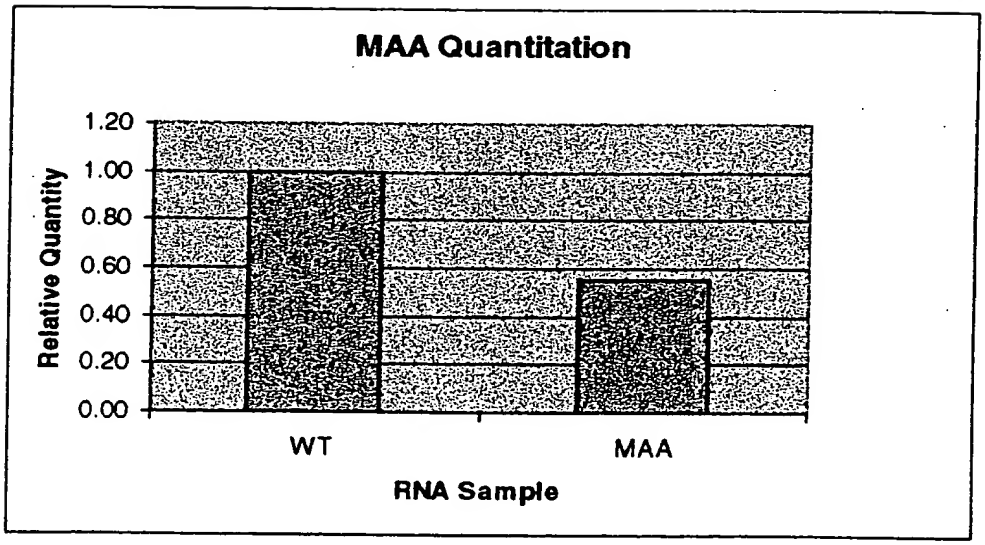


Inoculum for SAM2 was somewhat higher; at equal inocula growth of SAM2 single allele knock-out is slightly slower.

FIG. 79.

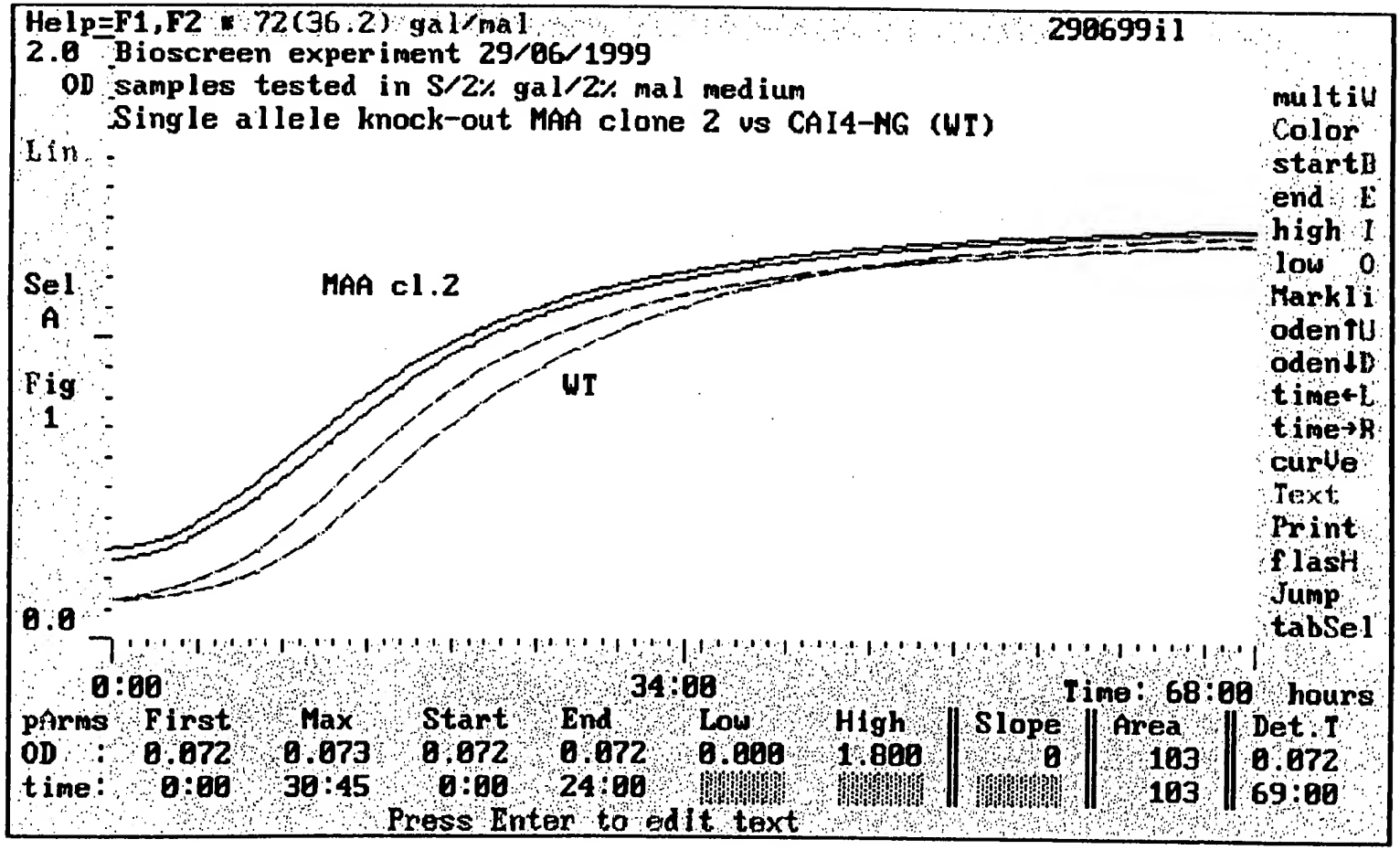
Relative quantitation for MAA vs. Act

	Avrg.MAA	Avrg. ACT	dCt	ddCt	2-ddct
WT	34.85	33.49	1.36	0.00	1.00
MAA	32.86	30.64	2.22	0.86	0.55



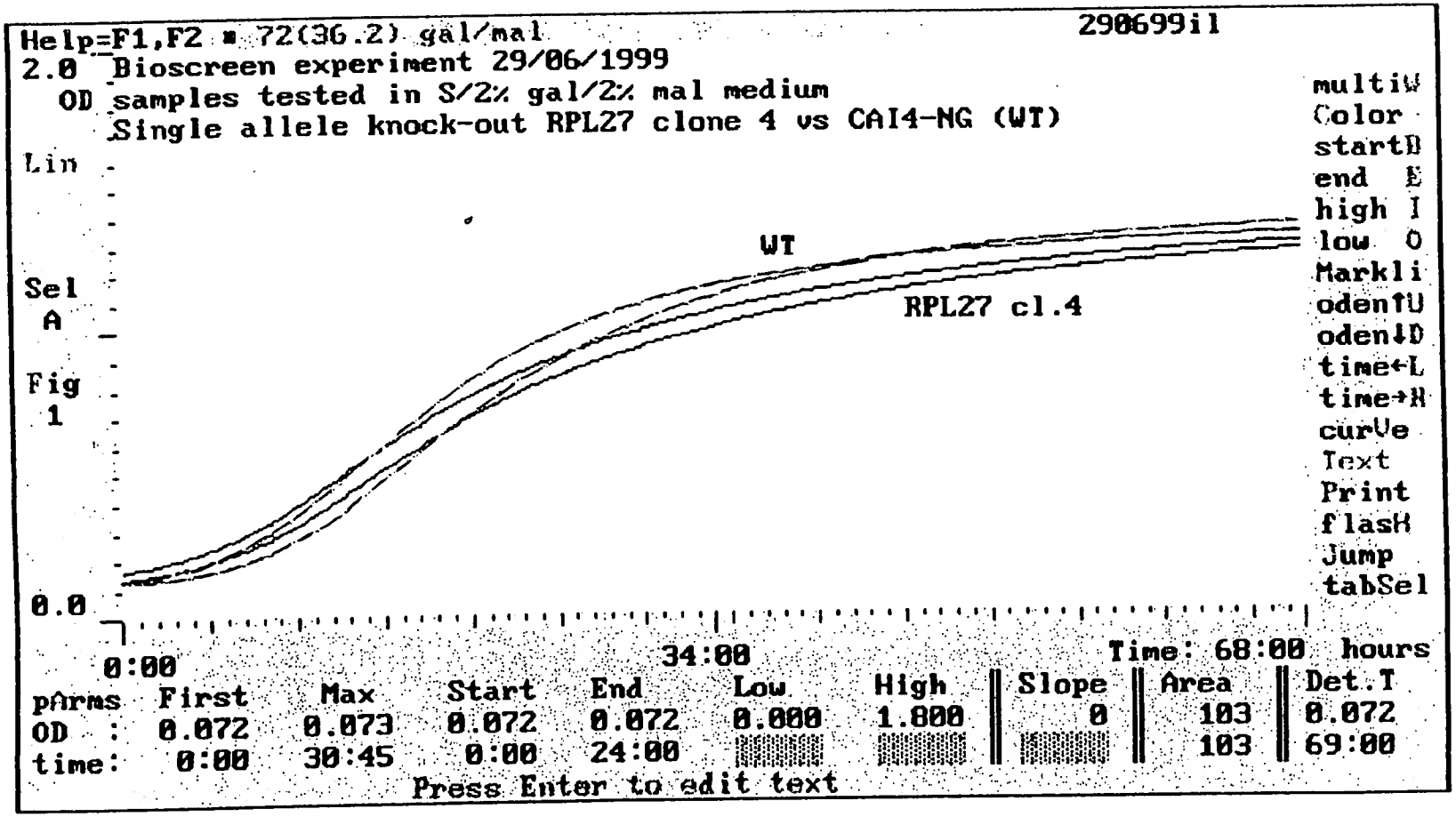
MAA expression was decreased two fold in the MAA knock-out compared to the Wt.

FIG. 80.



Inoculum for MAA was somewhat higher; at equal inocula growth of MAA single allele knock-out is slightly slower.

FIG. 82.

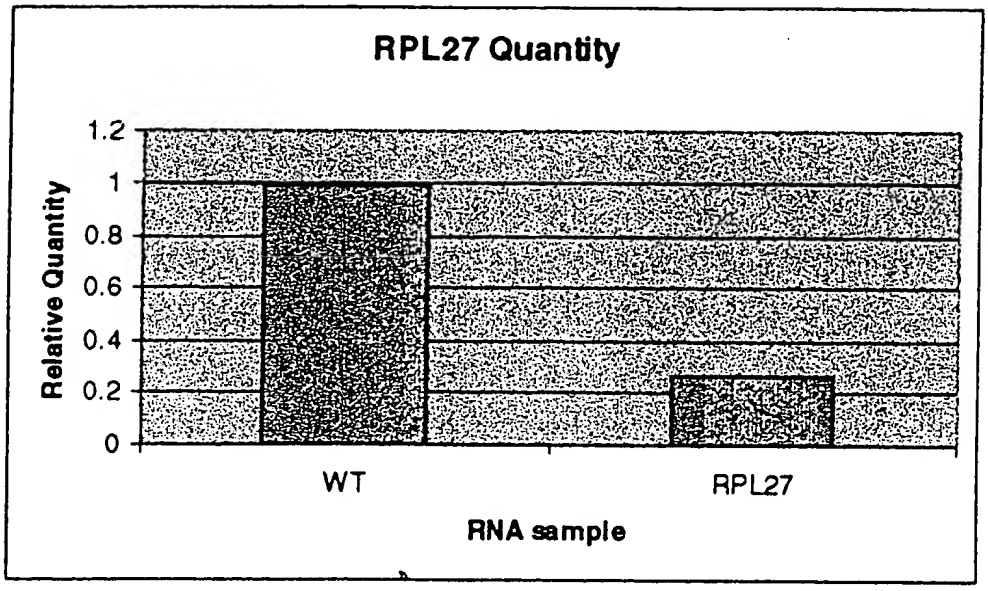


The RPL27 single allele knock-out grows equally to the wild type strain.

FIG. 81.

Relative quantitation for RPL27 vs. Act

	Avrg. RPL27	Avrg. ACT	dCt	ddCt	2-ddct
WT	33.01	33.49	-0.48	0.00	1
RPL27	34.37	32.98	1.39	1.87	0.27



RPL27 expression was decreased more than three fold in the RPL27 knock-out compared to the Wt.